GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 15:17:59 ; Search time 1605 Seconds
(without alignments)
294.640 Million cell updates/sec

Title: US-09-813-824A-3
Perfect score: 10
Sequence: 1 RRRCWWGYYY 10

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2172512

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	10	100.0	10	6	A67159	A67159 Sequence 16
c	2	10	100.0	10	6	A67159	A67159 Sequence 16
	3	10	100.0	10	6	AR003507	AR003507 Sequence
c	4	10	100.0	10	6	AR003507	AR003507 Sequence
	5	10	100.0	10	6	AR070749	AR070749 Sequence
c	6	10	100.0	10	6	AR070749	AR070749 Sequence
	7	10	100.0	10	6	AR074547	AR074547 Sequence
c	8	10	100.0	10	6	AR074547	AR074547 Sequence
	9	10	100.0	10	6	AR124219	AR124219 Sequence
c	10	10	100.0	10	6	AR124219	AR124219 Sequence
	11	10	100.0	10	6	AR157427	AR157427 Sequence
c	12	10	100.0	10	6	AR157427	AR157427 Sequence
	13	10	100.0	10	6	I62424	I62424 Sequence 30
c	14	10	100.0	10	6	I62424	I62424 Sequence 30
	15	10	100.0	10	6	AR303877	AR303877 Sequence
c	16	10	100.0	10	6	AR303877	AR303877 Sequence
	17	10	100.0	10	6	AX077262	AX077262 Sequence
c	18	10	100.0	10	6	AX077262	AX077262 Sequence
	19	10	100.0	10	6	AX339211	AX339211 Sequence
c	20	10	100.0	10	6	AX339211	AX339211 Sequence
	21	10	100.0	10	6	AX776278	AX776278 Sequence
c	22	10	100.0	10	6	AX776278	AX776278 Sequence
	23	10	100.0	10	6	AX803572	AX803572 Sequence
c	24	10	100.0	10	6	AX803572	AX803572 Sequence
	25	10	100.0	10	6	BD064950	BD064950 Method fo
c	26	10	100.0	10	6	BD064950	BD064950 Method fo
	27	10	100.0	10	6	BD084759	BD084759 Human ner
c	28	10	100.0	10	6	BD084759	BD084759 Human ner
	29	10	100.0	19	6	AX685336	AX685336 Sequence
c	30	10	100.0	19	6	AX685336	AX685336 Sequence
	31	10	100.0	20	6	AR181179	AR181179 Sequence
c	32	10	100.0	20	6	AR181179	AR181179 Sequence
	33	10	100.0	21	6	AR060431	AR060431 Sequence
c	34	10	100.0	21	6	AR060431	AR060431 Sequence
	35	5	50.0	20	6	I22646	I22646 Sequence 13
c	36	5	50.0	20	6	I22646	I22646 Sequence 13
	37	5	50.0	20	6	I47471	I47471 Sequence 13
c	38	5	50.0	20	6	I47471	I47471 Sequence 13
	39	4	40.0	10	6	CQ771564	CQ771564 Sequence
c	40	4	40.0	10	6	CQ771564	CQ771564 Sequence
	41	4	40.0	10	6	I74680	I74680 Sequence 9
c	42	4	40.0	10	6	I74680	I74680 Sequence 9
	43	4	40.0	10	6	I91766	I91766 Sequence 9
c	44	4	40.0	10	6	I91766	I91766 Sequence 9
	45	4	40.0	10	6	BD090936	BD090936 Method fo
c	46	4	40.0	10	6	BD090936	BD090936 Method fo
	47	4	40.0	12	6	BD084901	BD084901 Character
c	48	4	40.0	12	6	BD084901	BD084901 Character
	49	4	40.0	19	6	AR451567	AR451567 Sequence
c	50	4	40.0	19	6	AR451567	AR451567 Sequence
	51	4	40.0	19	6	AX412112	AX412112 Sequence
c	52	4	40.0	19	6	AX412112	AX412112 Sequence
	53	4	40.0	20	6	BD184677	BD184677 Method an
c	54	4	40.0	20	6	BD184677	BD184677 Method an
	55	4	40.0	20	6	I22645	I22645 Sequence 13
c	56	4	40.0	20	6	I22645	I22645 Sequence 13
	57	4	40.0	20	6	I22647	I22647 Sequence 13
c	58	4	40.0	20	6	I22647	I22647 Sequence 13
	59	4	40.0	20	6	I47470	I47470 Sequence 13
c	60	4	40.0	20	6	I47470	I47470 Sequence 13
	61	4	40.0	20	6	I47472	I47472 Sequence 13
c	62	4	40.0	20	6	I47472	I47472 Sequence 13
	63	4	40.0	27	6	AR030183	AR030183 Sequence
c	64	4	40.0	27	6	AR030183	AR030183 Sequence
	65	4	40.0	27	6	AR030187	AR030187 Sequence
c	66	4	40.0	27	6	AR030187	AR030187 Sequence
	67	4	40.0	27	6	AR140600	AR140600 Sequence
c	68	4	40.0	27	6	AR140600	AR140600 Sequence
	69	4	40.0	27	6	I17358	I17358 Sequence 8
c	70	4	40.0	27	6	I17358	I17358 Sequence 8
	71	4	40.0	27	6	I17359	I17359 Sequence 9
c	72	4	40.0	27	6	I17359	I17359 Sequence 9
	73	4	40.0	27	6	AR477281	AR477281 Sequence
c	74	4	40.0	27	6	AR477281	AR477281 Sequence
	75	4	40.0	27	6	AR477282	AR477282 Sequence
c	76	4	40.0	27	6	AR477282	AR477282 Sequence
	77	4	40.0	38	6	BD132388	BD132388 DNA diagn
c	78	4	40.0	38	6	BD132388	BD132388 DNA diagn
	79	4	40.0	42	6	AX328823	AX328823 Sequence
c	80	4	40.0	42	6	AX328823	AX328823 Sequence
	81	4	40.0	63	4	DOGSR7SL1	M30845 Dog signal
c	82	4	40.0	63	4	DOGSR7SL1	M30845 Dog signal
	83	3	30.0	6	6	A90866	A90866 Sequence 1
c	84	3	30.0	6	6	A90866	A90866 Sequence 1
	85	3	30.0	6	6	E64767	E64767 Chemically
c	86	3	30.0	6	6	E64767	E64767 Chemically
	87	3	30.0	6	6	AX797664	AX797664 Sequence
c	88	3	30.0	6	6	AX797664	AX797664 Sequence
	89	3	30.0	6	6	AX957648	AX957648 Sequence
c	90	3	30.0	6	6	AX957648	AX957648 Sequence
	91	3	30.0	6	6	AX957742	AX957742 Sequence
c	92	3	30.0	6	6	AX957742	AX957742 Sequence

93	3	30.0	6	6	AX958147	AX958147 Sequence
c 94	3	30.0	6	6	AX958147	AX958147 Sequence
95	3	30.0	7	6	BD211369	BD211369 Method of
c 96	3	30.0	7	6	BD211369	BD211369 Method of
97	3	30.0	7	6	BD211370	BD211370 Method of
c 98	3	30.0	7	6	BD211370	BD211370 Method of
99	3	30.0	8	6	E64766	E64766 Chemically
c 100	3	30.0	8	6	E64766	E64766 Chemically
101	3	30.0	8	6	AX046162	AX046162 Sequence
c 102	3	30.0	8	6	AX046162	AX046162 Sequence
103	3	30.0	8	6	BD084758	BD084758 Human ner
c 104	3	30.0	8	6	BD084758	BD084758 Human ner
105	3	30.0	10	6	A37861	A37861 Sequence 4
c 106	3	30.0	10	6	A37861	A37861 Sequence 4
107	3	30.0	10	6	AR074451	AR074451 Sequence
c 108	3	30.0	10	6	AR074451	AR074451 Sequence
109	3	30.0	10	6	AR081131	AR081131 Sequence
c 110	3	30.0	10	6	AR081131	AR081131 Sequence
111	3	30.0	10	6	AR085328	AR085328 Sequence
c 112	3	30.0	10	6	AR085328	AR085328 Sequence
113	3	30.0	10	6	AR088076	AR088076 Sequence
c 114	3	30.0	10	6	AR088076	AR088076 Sequence
115	3	30.0	10	6	AR104235	AR104235 Sequence
c 116	3	30.0	10	6	AR104235	AR104235 Sequence
117	3	30.0	10	6	AR110243	AR110243 Sequence
c 118	3	30.0	10	6	AR110243	AR110243 Sequence
119	3	30.0	10	6	AR134895	AR134895 Sequence
c 120	3	30.0	10	6	AR134895	AR134895 Sequence
121	3	30.0	10	6	AR139421	AR139421 Sequence
c 122	3	30.0	10	6	AR139421	AR139421 Sequence
123	3	30.0	10	6	AR143499	AR143499 Sequence
c 124	3	30.0	10	6	AR143499	AR143499 Sequence
125	3	30.0	10	6	AR170002	AR170002 Sequence
c 126	3	30.0	10	6	AR170002	AR170002 Sequence
127	3	30.0	10	6	AR171403	AR171403 Sequence
c 128	3	30.0	10	6	AR171403	AR171403 Sequence
129	3	30.0	10	6	AR171574	AR171574 Sequence
c 130	3	30.0	10	6	AR171574	AR171574 Sequence
131	3	30.0	10	6	AR171811	AR171811 Sequence
c 132	3	30.0	10	6	AR171811	AR171811 Sequence
133	3	30.0	10	6	BD189505	BD189505 PROMOTER
c 134	3	30.0	10	6	BD189505	BD189505 PROMOTER
135	3	30.0	10	6	BD243164	BD243164 MN gene a
c 136	3	30.0	10	6	BD243164	BD243164 MN gene a
137	3	30.0	10	6	CQ814915	CQ814915 Sequence
c 138	3	30.0	10	6	CQ814915	CQ814915 Sequence
139	3	30.0	10	6	I72403	I72403 Sequence 34
c 140	3	30.0	10	6	I72403	I72403 Sequence 34
141	3	30.0	10	6	I84595	I84595 Sequence 1
c 142	3	30.0	10	6	I84595	I84595 Sequence 1
143	3	30.0	10	6	I84606	I84606 Sequence 12
c 144	3	30.0	10	6	I84606	I84606 Sequence 12
145	3	30.0	10	6	AR220243	AR220243 Sequence
c 146	3	30.0	10	6	AR220243	AR220243 Sequence
147	3	30.0	10	6	AR264148	AR264148 Sequence
c 148	3	30.0	10	6	AR264148	AR264148 Sequence
149	3	30.0	10	6	AR362282	AR362282 Sequence
c 150	3	30.0	10	6	AR362282	AR362282 Sequence
151	3	30.0	10	6	AX412946	AX412946 Sequence
c 152	3	30.0	10	6	AX412946	AX412946 Sequence
153	3	30.0	10	6	AX497559	AX497559 Sequence
c 154	3	30.0	10	6	AX497559	AX497559 Sequence
155	3	30.0	10	6	BD009036	BD009036 Promoter
c 156	3	30.0	10	6	BD009036	BD009036 Promoter
157	3	30.0	10	6	BD063695	BD063695 Glutathio
c 158	3	30.0	10	6	BD063695	BD063695 Glutathio
159	3	30.0	10	6	BD073429	BD073429 Expressio
c 160	3	30.0	10	6	BD073429	BD073429 Expressio
161	3	30.0	10	6	BD091328	BD091328 In vitro
c 162	3	30.0	10	6	BD091328	BD091328 In vitro
163	3	30.0	11	6	I84607	I84607 Sequence 13
c 164	3	30.0	11	6	I84607	I84607 Sequence 13
165	3	30.0	11	6	AX012240	AX012240 Sequence
c 166	3	30.0	11	6	AX012240	AX012240 Sequence
167	3	30.0	11	6	AX711145	AX711145 Sequence
c 168	3	30.0	11	6	AX711145	AX711145 Sequence
169	3	30.0	11	6	AX711146	AX711146 Sequence
c 170	3	30.0	11	6	AX711146	AX711146 Sequence
171	3	30.0	11	6	AX711147	AX711147 Sequence
c 172	3	30.0	11	6	AX711147	AX711147 Sequence
173	3	30.0	11	6	AX711148	AX711148 Sequence
c 174	3	30.0	11	6	AX711148	AX711148 Sequence
175	3	30.0	12	6	I84596	I84596 Sequence 2
c 176	3	30.0	12	6	I84596	I84596 Sequence 2
177	3	30.0	12	6	I84608	I84608 Sequence 14
c 178	3	30.0	12	6	I84608	I84608 Sequence 14
179	3	30.0	12	6	AX412933	AX412933 Sequence
c 180	3	30.0	12	6	AX412933	AX412933 Sequence
181	3	30.0	12	6	AX816374	AX816374 Sequence
c 182	3	30.0	12	6	AX816374	AX816374 Sequence
183	3	30.0	12	6	AX816375	AX816375 Sequence
c 184	3	30.0	12	6	AX816375	AX816375 Sequence
185	3	30.0	12	6	BD074027	BD074027 Human gli
c 186	3	30.0	12	6	BD074027	BD074027 Human gli
187	3	30.0	13	6	I27012	I27012 Sequence 33
c 188	3	30.0	13	6	I27012	I27012 Sequence 33
189	3	30.0	13	6	I84597	I84597 Sequence 3
c 190	3	30.0	13	6	I84597	I84597 Sequence 3
191	3	30.0	13	6	I84609	I84609 Sequence 15
c 192	3	30.0	13	6	I84609	I84609 Sequence 15
193	3	30.0	13	6	AX235305	AX235305 Sequence
c 194	3	30.0	13	6	AX235305	AX235305 Sequence
195	3	30.0	14	6	AR134892	AR134892 Sequence
c 196	3	30.0	14	6	AR134892	AR134892 Sequence
197	3	30.0	14	6	AR138914	AR138914 Sequence
c 198	3	30.0	14	6	AR138914	AR138914 Sequence
199	3	30.0	14	6	AR156467	AR156467 Sequence
c 200	3	30.0	14	6	AR156467	AR156467 Sequence
201	3	30.0	14	6	BD211484	BD211484 Modifying
c 202	3	30.0	14	6	BD211484	BD211484 Modifying
203	3	30.0	14	6	BD221627	BD221627 Upstream
c 204	3	30.0	14	6	BD221627	BD221627 Upstream
205	3	30.0	14	6	BD222103	BD222103 Upstream
c 206	3	30.0	14	6	BD222103	BD222103 Upstream
207	3	30.0	14	6	I38794	I38794 Sequence 32
c 208	3	30.0	14	6	I38794	I38794 Sequence 32
209	3	30.0	14	6	I84598	I84598 Sequence 4
c 210	3	30.0	14	6	I84598	I84598 Sequence 4
211	3	30.0	14	6	I84610	I84610 Sequence 16
c 212	3	30.0	14	6	I84610	I84610 Sequence 16
213	3	30.0	14	6	AR287313	AR287313 Sequence
c 214	3	30.0	14	6	AR287313	AR287313 Sequence
215	3	30.0	14	6	AR339730	AR339730 Sequence
c 216	3	30.0	14	6	AR339730	AR339730 Sequence
217	3	30.0	14	6	AX711201	AX711201 Sequence
c 218	3	30.0	14	6	AX711201	AX711201 Sequence
219	3	30.0	14	6	BD174481	BD174481 DNA parti
c 220	3	30.0	14	6	BD174481	BD174481 DNA parti
221	3	30.0	15	6	AR076616	AR076616 Sequence
c 222	3	30.0	15	6	AR076616	AR076616 Sequence
223	3	30.0	15	6	AR094365	AR094365 Sequence
c 224	3	30.0	15	6	AR094365	AR094365 Sequence
225	3	30.0	15	6	I84599	I84599 Sequence 5
c 226	3	30.0	15	6	I84599	I84599 Sequence 5
227	3	30.0	15	6	I84611	I84611 Sequence 17
c 228	3	30.0	15	6	I84611	I84611 Sequence 17
229	3	30.0	15	6	AR399667	AR399667 Sequence
c 230	3	30.0	15	6	AR399667	AR399667 Sequence
231	3	30.0	15	6	AR477239	AR477239 Sequence
c 232	3	30.0	15	6	AR477239	AR477239 Sequence
233	3	30.0	16	6	AR010020	AR010020 Sequence
c 234	3	30.0	16	6	AR010020	AR010020 Sequence
235	3	30.0	16	6	AR034755	AR034755 Sequence
c 236	3	30.0	16	6	AR034755	AR034755 Sequence
237	3	30.0	16	6	BD272242	BD272242 Anti-angi
c 238	3	30.0	16	6	BD272242	BD272242 Anti-angi

239	3	30.0	16	6	E05701	E05701 Human VNTR
c 240	3	30.0	16	6	E05701	E05701 Human VNTR
241	3	30.0	16	6	I84600	I84600 Sequence 6
c 242	3	30.0	16	6	I84600	I84600 Sequence 6
243	3	30.0	16	6	I84612	I84612 Sequence 18
c 244	3	30.0	16	6	I84612	I84612 Sequence 18
245	3	30.0	16	6	AX063592	AX063592 Sequence
c 246	3	30.0	16	6	AX063592	AX063592 Sequence
247	3	30.0	16	6	BD007074	BD007074 IL-12 gen
c 248	3	30.0	16	6	BD007074	BD007074 IL-12 gen
249	3	30.0	16	6	BD007084	BD007084 Gene expr
c 250	3	30.0	16	6	BD007084	BD007084 Gene expr
251	3	30.0	16	6	BD069115	BD069115 IL-2 gene
c 252	3	30.0	16	6	BD069115	BD069115 IL-2 gene
253	3	30.0	16	6	BD136053	BD136053 Interfero
c 254	3	30.0	16	6	BD136053	BD136053 Interfero
255	3	30.0	17	6	A10145	A10145 Nucleotide
c 256	3	30.0	17	6	A10145	A10145 Nucleotide
257	3	30.0	17	6	AR179897	AR179897 Sequence
c 258	3	30.0	17	6	AR179897	AR179897 Sequence
259	3	30.0	17	6	BD178105	BD178105 On the st
c 260	3	30.0	17	6	BD178105	BD178105 On the st
261	3	30.0	17	6	BD231184	BD231184 Peptidyl-
c 262	3	30.0	17	6	BD231184	BD231184 Peptidyl-
263	3	30.0	17	6	BD242683	BD242683 Interleuk
c 264	3	30.0	17	6	BD242683	BD242683 Interleuk
265	3	30.0	17	6	BD264374	BD264374 Growth fa
c 266	3	30.0	17	6	BD264374	BD264374 Growth fa
267	3	30.0	17	6	BD276216	BD276216 GROWTH FA
c 268	3	30.0	17	6	BD276216	BD276216 GROWTH FA
269	3	30.0	17	6	I38773	I38773 Sequence 11
c 270	3	30.0	17	6	I38773	I38773 Sequence 11
271	3	30.0	17	6	I84601	I84601 Sequence 7
c 272	3	30.0	17	6	I84601	I84601 Sequence 7
273	3	30.0	17	6	I84613	I84613 Sequence 19
c 274	3	30.0	17	6	I84613	I84613 Sequence 19
275	3	30.0	17	6	AR182270	AR182270 Sequence
c 276	3	30.0	17	6	AR182270	AR182270 Sequence
277	3	30.0	17	6	AR267258	AR267258 Sequence
c 278	3	30.0	17	6	AR267258	AR267258 Sequence
279	3	30.0	17	6	AR282954	AR282954 Sequence
c 280	3	30.0	17	6	AR282954	AR282954 Sequence
281	3	30.0	17	6	AR305625	AR305625 Sequence
c 282	3	30.0	17	6	AR305625	AR305625 Sequence
283	3	30.0	17	6	AR341726	AR341726 Sequence
c 284	3	30.0	17	6	AR341726	AR341726 Sequence
285	3	30.0	17	6	AR371874	AR371874 Sequence
c 286	3	30.0	17	6	AR371874	AR371874 Sequence
287	3	30.0	17	6	AR381177	AR381177 Sequence
c 288	3	30.0	17	6	AR381177	AR381177 Sequence
289	3	30.0	17	6	AR411868	AR411868 Sequence
c 290	3	30.0	17	6	AR411868	AR411868 Sequence
291	3	30.0	17	6	AR451316	AR451316 Sequence
c 292	3	30.0	17	6	AR451316	AR451316 Sequence
293	3	30.0	17	6	AR451317	AR451317 Sequence
c 294	3	30.0	17	6	AR451317	AR451317 Sequence
295	3	30.0	17	6	AX024012	AX024012 Sequence
c 296	3	30.0	17	6	AX024012	AX024012 Sequence
297	3	30.0	17	6	AX044496	AX044496 Sequence
c 298	3	30.0	17	6	AX044496	AX044496 Sequence
299	3	30.0	17	6	BD013768	BD013768 ML-236B b
c 300	3	30.0	17	6	BD013768	BD013768 ML-236B b
301	3	30.0	17	6	BD093556	BD093556 DNAs rela
c 302	3	30.0	17	6	BD093556	BD093556 DNAs rela
303	3	30.0	17	6	BD130891	BD130891 Novel cys
c 304	3	30.0	17	6	BD130891	BD130891 Novel cys
305	3	30.0	18	6	AR169356	AR169356 Sequence
c 306	3	30.0	18	6	AR169356	AR169356 Sequence
307	3	30.0	18	6	I84602	I84602 Sequence 8
c 308	3	30.0	18	6	I84602	I84602 Sequence 8
309	3	30.0	18	6	I84614	I84614 Sequence 20
c 310	3	30.0	18	6	I84614	I84614 Sequence 20
311	3	30.0	18	6	AX019961	AX019961 Sequence
c 312	3	30.0	18	6	AX019961	AX019961 Sequence
313	3	30.0	18	6	AX361167	AX361167 Sequence
c 314	3	30.0	18	6	AX361167	AX361167 Sequence
315	3	30.0	18	6	BD013142	BD013142 A gene en
c 316	3	30.0	18	6	BD013142	BD013142 A gene en
317	3	30.0	19	6	I22648	I22648 Sequence 13
c 318	3	30.0	19	6	I22648	I22648 Sequence 13
319	3	30.0	19	6	I26989	I26989 Sequence 10
c 320	3	30.0	19	6	I26989	I26989 Sequence 10
321	3	30.0	19	6	I26990	I26990 Sequence 11
c 322	3	30.0	19	6	I26990	I26990 Sequence 11
323	3	30.0	19	6	I38772	I38772 Sequence 10
c 324	3	30.0	19	6	I38772	I38772 Sequence 10
325	3	30.0	19	6	I47473	I47473 Sequence 13
c 326	3	30.0	19	6	I47473	I47473 Sequence 13
327	3	30.0	19	6	I84603	I84603 Sequence 9
c 328	3	30.0	19	6	I84603	I84603 Sequence 9
329	3	30.0	19	6	AR451564	AR451564 Sequence
c 330	3	30.0	19	6	AR451564	AR451564 Sequence
331	3	30.0	19	6	AR451566	AR451566 Sequence
c 332	3	30.0	19	6	AR451566	AR451566 Sequence
333	3	30.0	19	6	AX412109	AX412109 Sequence
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335	3	30.0	19	6	AX412111	AX412111 Sequence
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337	3	30.0	19	6	AX521629	AX521629 Sequence
c 338	3	30.0	19	6	AX521629	AX521629 Sequence
339	3	30.0	20	6	E05812	E05812 PCR primer
c 340	3	30.0	20	6	E05812	E05812 PCR primer
341	3	30.0	20	6	E05814	E05814 PCR primer
c 342	3	30.0	20	6	E05814	E05814 PCR primer
343	3	30.0	20	6	E08450	E08450 DNA fragmen
c 344	3	30.0	20	6	E08450	E08450 DNA fragmen
345	3	30.0	20	6	E08451	E08451 DNA fragmen
c 346	3	30.0	20	6	E08451	E08451 DNA fragmen
347	3	30.0	20	6	E08909	E08909 Oligonucleo
c 348	3	30.0	20	6	E08909	E08909 Oligonucleo
349	3	30.0	20	6	E08911	E08911 Oligonucleo
c 350	3	30.0	20	6	E08911	E08911 Oligonucleo
351	3	30.0	20	6	E13751	E13751 PCR primer
c 352	3	30.0	20	6	E13751	E13751 PCR primer
353	3	30.0	20	6	I12595	I12595 Sequence 5
c 354	3	30.0	20	6	I12595	I12595 Sequence 5
355	3	30.0	20	6	I12597	I12597 Sequence 7
c 356	3	30.0	20	6	I12597	I12597 Sequence 7
357	3	30.0	20	6	I22642	I22642 Sequence 13
c 358	3	30.0	20	6	I22642	I22642 Sequence 13
359	3	30.0	20	6	I47467	I47467 Sequence 13
c 360	3	30.0	20	6	I47467	I47467 Sequence 13
361	3	30.0	20	6	I84604	I84604 Sequence 10
c 362	3	30.0	20	6	I84604	I84604 Sequence 10
363	3	30.0	20	6	AR305627	AR305627 Sequence
c 364	3	30.0	20	6	AR305627	AR305627 Sequence
365	3	30.0	20	6	AR408904	AR408904 Sequence
c 366	3	30.0	20	6	AR408904	AR408904 Sequence
367	3	30.0	20	6	AX076269	AX076269 Sequence
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369	3	30.0	20	6	AX076270	AX076270 Sequence
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371	3	30.0	20	6	AX081210	AX081210 Sequence
c 372	3	30.0	20	6	AX081210	AX081210 Sequence
373	3	30.0	20	6	AX098625	AX098625 Sequence
c 374	3	30.0	20	6	AX098625	AX098625 Sequence
375	3	30.0	20	6	AX110203	AX110203 Sequence
c 376	3	30.0	20	6	AX110203	AX110203 Sequence
377	3	30.0	20	6	AX167403	AX167403 Sequence
c 378	3	30.0	20	6	AX167403	AX167403 Sequence
379	3	30.0	20	6	AX250520	AX250520 Sequence
c 380	3	30.0	20	6	AX250520	AX250520 Sequence
381	3	30.0	20	6	AX716737	AX716737 Sequence
c 382	3	30.0	20	6	AX716737	AX716737 Sequence
383	3	30.0	20	6	AX719245	AX719245 Sequence
c 384	3	30.0	20	6	AX719245	AX719245 Sequence

385	3	30.0	21	6	A07255	A07255 Oligonucleo
c 386	3	30.0	21	6	A07255	A07255 Oligonucleo
387	3	30.0	21	6	AR169411	AR169411 Sequence
c 388	3	30.0	21	6	AR169411	AR169411 Sequence
389	3	30.0	21	6	AR169413	AR169413 Sequence
c 390	3	30.0	21	6	AR169413	AR169413 Sequence
391	3	30.0	21	6	AR169442	AR169442 Sequence
c 392	3	30.0	21	6	AR169442	AR169442 Sequence
393	3	30.0	21	6	AR169444	AR169444 Sequence
c 394	3	30.0	21	6	AR169444	AR169444 Sequence
395	3	30.0	21	6	BD231011	BD231011 Mammalian
c 396	3	30.0	21	6	BD231011	BD231011 Mammalian
397	3	30.0	21	6	I22810	I22810 Sequence 29
c 398	3	30.0	21	6	I22810	I22810 Sequence 29
399	3	30.0	21	6	I47635	I47635 Sequence 29
c 400	3	30.0	21	6	I47635	I47635 Sequence 29
401	3	30.0	21	6	AX711231	AX711231 Sequence
c 402	3	30.0	21	6	AX711231	AX711231 Sequence
403	3	30.0	21	6	AX774486	AX774486 Sequence
c 404	3	30.0	21	6	AX774486	AX774486 Sequence
405	3	30.0	21	6	AX955618	AX955618 Sequence
c 406	3	30.0	21	6	AX955618	AX955618 Sequence
407	3	30.0	21	6	BD085429	BD085429 Method fo
c 408	3	30.0	21	6	BD085429	BD085429 Method fo
409	3	30.0	21	6	BD085435	BD085435 Method fo
c 410	3	30.0	21	6	BD085435	BD085435 Method fo
411	3	30.0	22	6	A65929	A65929 Sequence 5
c 412	3	30.0	22	6	A65929	A65929 Sequence 5
413	3	30.0	22	6	AR168703	AR168703 Sequence
c 414	3	30.0	22	6	AR168703	AR168703 Sequence
415	3	30.0	22	6	AX003361	AX003361 Sequence
c 416	3	30.0	22	6	AX003361	AX003361 Sequence
417	3	30.0	23	6	A19190	A19190 Markush oli
c 418	3	30.0	23	6	A19190	A19190 Markush oli
419	3	30.0	23	6	AR032167	AR032167 Sequence
c 420	3	30.0	23	6	AR032167	AR032167 Sequence
421	3	30.0	23	6	AR145983	AR145983 Sequence
c 422	3	30.0	23	6	AR145983	AR145983 Sequence
423	3	30.0	23	6	AR169397	AR169397 Sequence
c 424	3	30.0	23	6	AR169397	AR169397 Sequence
425	3	30.0	23	6	AR169399	AR169399 Sequence
c 426	3	30.0	23	6	AR169399	AR169399 Sequence
427	3	30.0	23	6	BD188516	BD188516 Method fo
c 428	3	30.0	23	6	BD188516	BD188516 Method fo
429	3	30.0	23	6	CQ778460	CQ778460 Sequence
c 430	3	30.0	23	6	CQ778460	CQ778460 Sequence
431	3	30.0	23	6	E51219	E51219 Disease tol
c 432	3	30.0	23	6	E51219	E51219 Disease tol
433	3	30.0	23	6	AR180874	AR180874 Sequence
c 434	3	30.0	23	6	AR180874	AR180874 Sequence
435	3	30.0	23	6	AX181866	AX181866 Sequence
c 436	3	30.0	23	6	AX181866	AX181866 Sequence
437	3	30.0	23	6	AX181973	AX181973 Sequence
c 438	3	30.0	23	6	AX181973	AX181973 Sequence
439	3	30.0	23	6	AX250634	AX250634 Sequence
c 440	3	30.0	23	6	AX250634	AX250634 Sequence
441	3	30.0	23	6	AX392031	AX392031 Sequence
c 442	3	30.0	23	6	AX392031	AX392031 Sequence
443	3	30.0	23	6	BD077266	BD077266 Method an
c 444	3	30.0	23	6	BD077266	BD077266 Method an
445	3	30.0	23	6	BD103211	BD103211 Factors i
c 446	3	30.0	23	6	BD103211	BD103211 Factors i
447	3	30.0	23	6	BD144117	BD144117 DNA marke
c 448	3	30.0	23	6	BD144117	BD144117 DNA marke
449	3	30.0	24	6	A32253	A32253 Synthetic M
c 450	3	30.0	24	6	A32253	A32253 Synthetic M
451	3	30.0	24	6	AR109608	AR109608 Sequence
c 452	3	30.0	24	6	AR109608	AR109608 Sequence
453	3	30.0	24	6	AR109806	AR109806 Sequence
c 454	3	30.0	24	6	AR109806	AR109806 Sequence
455	3	30.0	24	6	E12479	E12479 PCR primer
c 456	3	30.0	24	6	E12479	E12479 PCR primer
457	3	30.0	24	6	E47132	E47132 Protein fro
c 458	3	30.0	24	6	E47132	E47132 Protein fro
459	3	30.0	24	6	AR300918	AR300918 Sequence
c 460	3	30.0	24	6	AR300918	AR300918 Sequence
461	3	30.0	24	6	AR490304	AR490304 Sequence
c 462	3	30.0	24	6	AR490304	AR490304 Sequence
463	3	30.0	24	6	AX019962	AX019962 Sequence
c 464	3	30.0	24	6	AX019962	AX019962 Sequence
465	3	30.0	25	6	AR030182	AR030182 Sequence
c 466	3	30.0	25	6	AR030182	AR030182 Sequence
467	3	30.0	25	6	AR065198	AR065198 Sequence
c 468	3	30.0	25	6	AR065198	AR065198 Sequence
469	3	30.0	25	6	I17357	I17357 Sequence 7
c 470	3	30.0	25	6	I17357	I17357 Sequence 7
471	3	30.0	25	6	AR322479	AR322479 Sequence
c 472	3	30.0	25	6	AR322479	AR322479 Sequence
473	3	30.0	25	6	AR477280	AR477280 Sequence
c 474	3	30.0	25	6	AR477280	AR477280 Sequence
475	3	30.0	25	6	AX300979	AX300979 Sequence
c 476	3	30.0	25	6	AX300979	AX300979 Sequence
477	3	30.0	25	6	AX300995	AX300995 Sequence
c 478	3	30.0	25	6	AX300995	AX300995 Sequence
479	3	30.0	25	6	BD003196	BD003196 HPPD gene
c 480	3	30.0	25	6	BD003196	BD003196 HPPD gene
481	3	30.0	25	6	BD003199	BD003199 HPPD gene
c 482	3	30.0	25	6	BD003199	BD003199 HPPD gene
483	3	30.0	26	6	A23804	A23804 Artificial
c 484	3	30.0	26	6	A23804	A23804 Artificial
485	3	30.0	26	6	AR061661	AR061661 Sequence
c 486	3	30.0	26	6	AR061661	AR061661 Sequence
487	3	30.0	26	6	AR108560	AR108560 Sequence
c 488	3	30.0	26	6	AR108560	AR108560 Sequence
489	3	30.0	26	6	AR140606	AR140606 Sequence
c 490	3	30.0	26	6	AR140606	AR140606 Sequence
491	3	30.0	26	6	AR140991	AR140991 Sequence
c 492	3	30.0	26	6	AR140991	AR140991 Sequence
493	3	30.0	26	6	I16517	I16517 Sequence 34
c 494	3	30.0	26	6	I16517	I16517 Sequence 34
495	3	30.0	26	6	I17360	I17360 Sequence 10
c 496	3	30.0	26	6	I17360	I17360 Sequence 10
497	3	30.0	26	6	I67003	I67003 Sequence 34
c 498	3	30.0	26	6	I67003	I67003 Sequence 34
499	3	30.0	26	6	I85097	I85097 Sequence 34
c 500	3	30.0	26	6	I85097	I85097 Sequence 34
501	3	30.0	26	6	AR263521	AR263521 Sequence
c 502	3	30.0	26	6	AR263521	AR263521 Sequence
503	3	30.0	26	6	AR477283	AR477283 Sequence
c 504	3	30.0	26	6	AR477283	AR477283 Sequence
505	3	30.0	26	6	AX109901	AX109901 Sequence
c 506	3	30.0	26	6	AX109901	AX109901 Sequence
507	3	30.0	26	6	AX363332	AX363332 Sequence
c 508	3	30.0	26	6	AX363332	AX363332 Sequence
509	3	30.0	26	6	AX443035	AX443035 Sequence
c 510	3	30.0	26	6	AX443035	AX443035 Sequence
511	3	30.0	26	6	AX443036	AX443036 Sequence
c 512	3	30.0	26	6	AX443036	AX443036 Sequence
513	3	30.0	26	6	BD080417	BD080417 Direct qu
c 514	3	30.0	26	6	BD080417	BD080417 Direct qu
515	3	30.0	27	6	AR061655	AR061655 Sequence
c 516	3	30.0	27	6	AR061655	AR061655 Sequence
517	3	30.0	27	6	AR108554	AR108554 Sequence
c 518	3	30.0	27	6	AR108554	AR108554 Sequence
519	3	30.0	27	6	AR117011	AR117011 Sequence
c 520	3	30.0	27	6	AR117011	AR117011 Sequence
521	3	30.0	27	6	AR140599	AR140599 Sequence
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523	3	30.0	27	6	AR140990	AR140990 Sequence
c 524	3	30.0	27	6	AR140990	AR140990 Sequence
525	3	30.0	27	6	BD195163	BD195163 CXCR3 che
c 526	3	30.0	27	6	BD195163	BD195163 CXCR3 che
527	3	30.0	27	6	E38902	E38902 Chimeric an
c 528	3	30.0	27	6	E38902	E38902 Chimeric an
529	3	30.0	27	6	I16511	I16511 Sequence 33
c 530	3	30.0	27	6	I16511	I16511 Sequence 33

531	3	30.0	27	6	I66997	I66997 Sequence 33
c 532	3	30.0	27	6	I66997	I66997 Sequence 33
533	3	30.0	27	6	I85091	I85091 Sequence 33
c 534	3	30.0	27	6	I85091	I85091 Sequence 33
535	3	30.0	27	6	AR263515	AR263515 Sequence
c 536	3	30.0	27	6	AR263515	AR263515 Sequence
537	3	30.0	27	6	AR409564	AR409564 Sequence
c 538	3	30.0	27	6	AR409564	AR409564 Sequence
539	3	30.0	27	6	AR443097	AR443097 Sequence
c 540	3	30.0	27	6	AR443097	AR443097 Sequence
541	3	30.0	27	6	AR456182	AR456182 Sequence
c 542	3	30.0	27	6	AR456182	AR456182 Sequence
543	3	30.0	27	6	AX068016	AX068016 Sequence
c 544	3	30.0	27	6	AX068016	AX068016 Sequence
545	3	30.0	28	6	AX278295	AX278295 Sequence
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547	3	30.0	28	6	AX428390	AX428390 Sequence
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549	3	30.0	28	6	AX823605	AX823605 Sequence
c 550	3	30.0	28	6	AX823605	AX823605 Sequence
551	3	30.0	29	6	AR061660	AR061660 Sequence
c 552	3	30.0	29	6	AR061660	AR061660 Sequence
553	3	30.0	29	6	AR108559	AR108559 Sequence
c 554	3	30.0	29	6	AR108559	AR108559 Sequence
555	3	30.0	29	6	CQ813531	CQ813531 Sequence
c 556	3	30.0	29	6	CQ813531	CQ813531 Sequence
557	3	30.0	29	6	I16516	I16516 Sequence 34
c 558	3	30.0	29	6	I16516	I16516 Sequence 34
559	3	30.0	29	6	I17750	I17750 Sequence 25
c 560	3	30.0	29	6	I17750	I17750 Sequence 25
561	3	30.0	29	6	I67002	I67002 Sequence 34
c 562	3	30.0	29	6	I67002	I67002 Sequence 34
563	3	30.0	29	6	I85096	I85096 Sequence 34
c 564	3	30.0	29	6	I85096	I85096 Sequence 34
565	3	30.0	29	6	AR213667	AR213667 Sequence
c 566	3	30.0	29	6	AR213667	AR213667 Sequence
567	3	30.0	29	6	AR263520	AR263520 Sequence
c 568	3	30.0	29	6	AR263520	AR263520 Sequence
569	3	30.0	29	6	BD057726	BD057726 Fusion pr
c 570	3	30.0	29	6	BD057726	BD057726 Fusion pr
571	3	30.0	29	6	BD081556	BD081556 Soluble s
c 572	3	30.0	29	6	BD081556	BD081556 Soluble s
573	3	30.0	30	6	A62994	A62994 Sequence 6
c 574	3	30.0	30	6	A62994	A62994 Sequence 6
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c 576	3	30.0	30	6	AR000084	AR000084 Sequence
577	3	30.0	30	6	AR064907	AR064907 Sequence
c 578	3	30.0	30	6	AR064907	AR064907 Sequence
579	3	30.0	30	6	BD184673	BD184673 Method an
c 580	3	30.0	30	6	BD184673	BD184673 Method an
581	3	30.0	30	6	AX190506	AX190506 Sequence
c 582	3	30.0	30	6	AX190506	AX190506 Sequence
583	3	30.0	30	6	BD091329	BD091329 In vitro
c 584	3	30.0	30	6	BD091329	BD091329 In vitro
585	3	30.0	30	6	BD095227	BD095227 Polypepti
c 586	3	30.0	30	6	BD095227	BD095227 Polypepti
587	3	30.0	31	6	AR035919	AR035919 Sequence
c 588	3	30.0	31	6	AR035919	AR035919 Sequence
589	3	30.0	31	6	I20155	I20155 Sequence 11
c 590	3	30.0	31	6	I20155	I20155 Sequence 11
591	3	30.0	31	6	AR340333	AR340333 Sequence
c 592	3	30.0	31	6	AR340333	AR340333 Sequence
593	3	30.0	32	6	AX591060	AX591060 Sequence
c 594	3	30.0	32	6	AX591060	AX591060 Sequence
595	3	30.0	32	6	AX810857	AX810857 Sequence
c 596	3	30.0	32	6	AX810857	AX810857 Sequence
597	3	30.0	32	6	BD087264	BD087264 Hyalurona
c 598	3	30.0	32	6	BD087264	BD087264 Hyalurona
599	3	30.0	33	6	AR004352	AR004352 Sequence
c 600	3	30.0	33	6	AR004352	AR004352 Sequence
601	3	30.0	33	6	AR004371	AR004371 Sequence
c 602	3	30.0	33	6	AR004371	AR004371 Sequence
603	3	30.0	33	6	AR004374	AR004374 Sequence
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609	3	30.0	33	6	AR097162	AR097162 Sequence
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613	3	30.0	33	6	AR097175	AR097175 Sequence
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617	3	30.0	33	6	AR130641	AR130641 Sequence
c 618	3	30.0	33	6	AR130641	AR130641 Sequence
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c 620	3	30.0	33	6	AR130660	AR130660 Sequence
621	3	30.0	33	6	AR130663	AR130663 Sequence
c 622	3	30.0	33	6	AR130663	AR130663 Sequence
623	3	30.0	33	6	AR130673	AR130673 Sequence
c 624	3	30.0	33	6	AR130673	AR130673 Sequence
625	3	30.0	33	6	AR147201	AR147201 Sequence
c 626	3	30.0	33	6	AR147201	AR147201 Sequence
627	3	30.0	33	6	AR171990	AR171990 Sequence
c 628	3	30.0	33	6	AR171990	AR171990 Sequence
629	3	30.0	33	6	AR172009	AR172009 Sequence
c 630	3	30.0	33	6	AR172009	AR172009 Sequence
631	3	30.0	33	6	AR172012	AR172012 Sequence
c 632	3	30.0	33	6	AR172012	AR172012 Sequence
633	3	30.0	33	6	AR172022	AR172022 Sequence
c 634	3	30.0	33	6	AR172022	AR172022 Sequence
635	3	30.0	33	6	BD189107	BD189107 HCV Genom
c 636	3	30.0	33	6	BD189107	BD189107 HCV Genom
637	3	30.0	33	6	BD189126	BD189126 HCV Genom
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639	3	30.0	33	6	BD189129	BD189129 HCV Genom
c 640	3	30.0	33	6	BD189129	BD189129 HCV Genom
641	3	30.0	33	6	BD189139	BD189139 HCV Genom
c 642	3	30.0	33	6	BD189139	BD189139 HCV Genom
643	3	30.0	33	6	BD189254	BD189254 HCV Genom
c 644	3	30.0	33	6	BD189254	BD189254 HCV Genom
645	3	30.0	33	6	BD189273	BD189273 HCV Genom
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647	3	30.0	33	6	BD189276	BD189276 HCV Genom
c 648	3	30.0	33	6	BD189276	BD189276 HCV Genom
649	3	30.0	33	6	BD189286	BD189286 HCV Genom
c 650	3	30.0	33	6	BD189286	BD189286 HCV Genom
651	3	30.0	33	6	BD189401	BD189401 HCV Genom
c 652	3	30.0	33	6	BD189401	BD189401 HCV Genom
653	3	30.0	33	6	BD189420	BD189420 HCV Genom
c 654	3	30.0	33	6	BD189420	BD189420 HCV Genom
655	3	30.0	33	6	BD189423	BD189423 HCV Genom
c 656	3	30.0	33	6	BD189423	BD189423 HCV Genom
657	3	30.0	33	6	BD189433	BD189433 HCV Genom
c 658	3	30.0	33	6	BD189433	BD189433 HCV Genom
659	3	30.0	33	6	I11453	I11453 Sequence 7
c 660	3	30.0	33	6	I11453	I11453 Sequence 7
661	3	30.0	33	6	I11457	I11457 Sequence 11
c 662	3	30.0	33	6	I11457	I11457 Sequence 11
663	3	30.0	33	6	I82827	I82827 Sequence 6
c 664	3	30.0	33	6	I82827	I82827 Sequence 6
665	3	30.0	33	6	I82846	I82846 Sequence 25
c 666	3	30.0	33	6	I82846	I82846 Sequence 25
667	3	30.0	33	6	I82849	I82849 Sequence 28
c 668	3	30.0	33	6	I82849	I82849 Sequence 28
669	3	30.0	33	6	I82859	I82859 Sequence 38
c 670	3	30.0	33	6	I82859	I82859 Sequence 38
671	3	30.0	33	6	AR202452	AR202452 Sequence
c 672	3	30.0	33	6	AR202452	AR202452 Sequence
673	3	30.0	33	6	AR368953	AR368953 Sequence
c 674	3	30.0	33	6	AR368953	AR368953 Sequence
675	3	30.0	33	6	AR368967	AR368967 Sequence
c 676	3	30.0	33	6	AR368967	AR368967 Sequence

677	3	30.0	33	6	AR369007	AR369007 Sequence
c 678	3	30.0	33	6	AR369007	AR369007 Sequence
679	3	30.0	33	6	AX190505	AX190505 Sequence
c 680	3	30.0	33	6	AX190505	AX190505 Sequence
681	3	30.0	33	6	BD010985	BD010985 HIV probe
c 682	3	30.0	33	6	BD010985	BD010985 HIV probe
683	3	30.0	33	6	BD010999	BD010999 HIV probe
c 684	3	30.0	33	6	BD010999	BD010999 HIV probe
685	3	30.0	33	6	BD011039	BD011039 HIV probe
c 686	3	30.0	33	6	BD011039	BD011039 HIV probe
687	3	30.0	34	6	AR150579	AR150579 Sequence
c 688	3	30.0	34	6	AR150579	AR150579 Sequence
689	3	30.0	34	6	AR350422	AR350422 Sequence
c 690	3	30.0	34	6	AR350422	AR350422 Sequence
691	3	30.0	34	6	AX955659	AX955659 Sequence
c 692	3	30.0	34	6	AX955659	AX955659 Sequence
693	3	30.0	35	6	AR156618	AR156618 Sequence
c 694	3	30.0	35	6	AR156618	AR156618 Sequence
695	3	30.0	35	6	E51753	E51753 Xylitol deh
c 696	3	30.0	35	6	E51753	E51753 Xylitol deh
697	3	30.0	35	6	AX739899	AX739899 Sequence
c 698	3	30.0	35	6	AX739899	AX739899 Sequence
699	3	30.0	35	6	AX781539	AX781539 Sequence
c 700	3	30.0	35	6	AX781539	AX781539 Sequence
701	3	30.0	35	6	AX817048	AX817048 Sequence
c 702	3	30.0	35	6	AX817048	AX817048 Sequence
703	3	30.0	36	6	AR013848	AR013848 Sequence
c 704	3	30.0	36	6	AR013848	AR013848 Sequence
705	3	30.0	36	6	AR033802	AR033802 Sequence
c 706	3	30.0	36	6	AR033802	AR033802 Sequence
707	3	30.0	36	6	AR042462	AR042462 Sequence
c 708	3	30.0	36	6	AR042462	AR042462 Sequence
709	3	30.0	36	6	AR058342	AR058342 Sequence
c 710	3	30.0	36	6	AR058342	AR058342 Sequence
711	3	30.0	36	6	AR060737	AR060737 Sequence
c 712	3	30.0	36	6	AR060737	AR060737 Sequence
713	3	30.0	36	6	AR068866	AR068866 Sequence
c 714	3	30.0	36	6	AR068866	AR068866 Sequence
715	3	30.0	36	6	AR088168	AR088168 Sequence
c 716	3	30.0	36	6	AR088168	AR088168 Sequence
717	3	30.0	37	6	AR024214	AR024214 Sequence
c 718	3	30.0	37	6	AR024214	AR024214 Sequence
719	3	30.0	38	6	CQ821249	CQ821249 Sequence
c 720	3	30.0	38	6	CQ821249	CQ821249 Sequence
721	3	30.0	38	6	AR302751	AR302751 Sequence
c 722	3	30.0	38	6	AR302751	AR302751 Sequence
723	3	30.0	38	6	AX078765	AX078765 Sequence
c 724	3	30.0	38	6	AX078765	AX078765 Sequence
725	3	30.0	38	6	AX361208	AX361208 Sequence
c 726	3	30.0	38	6	AX361208	AX361208 Sequence
727	3	30.0	39	6	I44118	I44118 Sequence 5
c 728	3	30.0	39	6	I44118	I44118 Sequence 5
729	3	30.0	39	6	I48966	I48966 Sequence 5
c 730	3	30.0	39	6	I48966	I48966 Sequence 5
731	3	30.0	39	6	AR302246	AR302246 Sequence
c 732	3	30.0	39	6	AR302246	AR302246 Sequence
733	3	30.0	39	6	AR367375	AR367375 Sequence
c 734	3	30.0	39	6	AR367375	AR367375 Sequence
735	3	30.0	39	6	AR367379	AR367379 Sequence
c 736	3	30.0	39	6	AR367379	AR367379 Sequence
737	3	30.0	39	6	AX080329	AX080329 Sequence
c 738	3	30.0	39	6	AX080329	AX080329 Sequence
739	3	30.0	41	6	AX518947	AX518947 Sequence
c 740	3	30.0	41	6	AX518947	AX518947 Sequence
741	3	30.0	41	6	AX518948	AX518948 Sequence
c 742	3	30.0	41	6	AX518948	AX518948 Sequence
743	3	30.0	42	6	AR110339	AR110339 Sequence
c 744	3	30.0	42	6	AR110339	AR110339 Sequence
745	3	30.0	42	6	AR263795	AR263795 Sequence
c 746	3	30.0	42	6	AR263795	AR263795 Sequence
747	3	30.0	42	6	BD009359	BD009359 Chimeric,
c 748	3	30.0	42	6	BD009359	BD009359 Chimeric,
749	3	30.0	45	6	AR145060	AR145060 Sequence
c 750	3	30.0	45	6	AR145060	AR145060 Sequence
751	3	30.0	45	6	AR145061	AR145061 Sequence
c 752	3	30.0	45	6	AR145061	AR145061 Sequence
753	3	30.0	45	6	AR145065	AR145065 Sequence
c 754	3	30.0	45	6	AR145065	AR145065 Sequence
755	3	30.0	47	6	AR292054	AR292054 Sequence
c 756	3	30.0	47	6	AR292054	AR292054 Sequence
757	3	30.0	48	6	AR028338	AR028338 Sequence
c 758	3	30.0	48	6	AR028338	AR028338 Sequence
759	3	30.0	48	6	I24936	I24936 Sequence 8
c 760	3	30.0	48	6	I24936	I24936 Sequence 8
761	3	30.0	48	6	AR233640	AR233640 Sequence
c 762	3	30.0	48	6	AR233640	AR233640 Sequence
763	3	30.0	50	6	AR428987	AR428987 Sequence
c 764	3	30.0	50	6	AR428987	AR428987 Sequence
765	3	30.0	51	6	AR321782	AR321782 Sequence
c 766	3	30.0	51	6	AR321782	AR321782 Sequence
767	3	30.0	51	6	AX911772	AX911772 Sequence
c 768	3	30.0	51	6	AX911772	AX911772 Sequence
769	3	30.0	51	6	BD047305	BD047305 Sequence
c 770	3	30.0	51	6	BD047305	BD047305 Sequence
771	3	30.0	54	6	E37139	E37139 Method for
c 772	3	30.0	54	6	E37139	E37139 Method for
773	3	30.0	54	6	E37140	E37140 Method for
c 774	3	30.0	54	6	E37140	E37140 Method for
775	3	30.0	58	6	AR417144	AR417144 Sequence
c 776	3	30.0	58	6	AR417144	AR417144 Sequence
777	3	30.0	58	6	AX914166	AX914166 Sequence
c 778	3	30.0	58	6	AX914166	AX914166 Sequence
779	3	30.0	58	6	AX977838	AX977838 Sequence
c 780	3	30.0	58	6	AX977838	AX977838 Sequence
781	3	30.0	58	6	BD049699	BD049699 Sequence
c 782	3	30.0	58	6	BD049699	BD049699 Sequence
783	3	30.0	58	6	BD112697	BD112697 EST and e
c 784	3	30.0	58	6	BD112697	BD112697 EST and e
785	3	30.0	59	6	AR023546	AR023546 Sequence
c 786	3	30.0	59	6	AR023546	AR023546 Sequence
787	3	30.0	59	6	AR082654	AR082654 Sequence
c 788	3	30.0	59	6	AR082654	AR082654 Sequence
789	3	30.0	59	6	AR156181	AR156181 Sequence
c 790	3	30.0	59	6	AR156181	AR156181 Sequence
791	3	30.0	59	6	AR381063	AR381063 Sequence
c 792	3	30.0	59	6	AR381063	AR381063 Sequence
793	3	30.0	60	6	A62989	A62989 Sequence 1
c 794	3	30.0	60	6	A62989	A62989 Sequence 1
795	3	30.0	61	6	AR165812	AR165812 Sequence
c 796	3	30.0	61	6	AR165812	AR165812 Sequence
797	3	30.0	61	6	AR305008	AR305008 Sequence
c 798	3	30.0	61	6	AR305008	AR305008 Sequence
799	3	30.0	61	6	AR423257	AR423257 Sequence
c 800	3	30.0	61	6	AR423257	AR423257 Sequence
801	3	30.0	61	6	AX983951	AX983951 Sequence
c 802	3	30.0	61	6	AX983951	AX983951 Sequence
803	3	30.0	61	6	BD118810	BD118810 EST and e
c 804	3	30.0	61	6	BD118810	BD118810 EST and e
805	3	30.0	63	6	AR393459	AR393459 Sequence
c 806	3	30.0	63	6	AR393459	AR393459 Sequence
807	3	30.0	64	6	AX909809	AX909809 Sequence
c 808	3	30.0	64	6	AX909809	AX909809 Sequence
809	3	30.0	64	6	BD045342	BD045342 Sequence
c 810	3	30.0	64	6	BD045342	BD045342 Sequence
811	3	30.0	66	6	A03733	A03733 Nucleotide
c 812	3	30.0	66	6	A03733	A03733 Nucleotide
813	3	30.0	68	6	AX900764	AX900764 Sequence
c 814	3	30.0	68	6	AX900764	AX900764 Sequence
815	3	30.0	68	6	BD036297	BD036297 Sequence
c 816	3	30.0	68	6	BD036297	BD036297 Sequence
817	3	30.0	69	6	AR149415	AR149415 Sequence
c 818	3	30.0	69	6	AR149415	AR149415 Sequence
819	3	30.0	69	6	AR149416	AR149416 Sequence
c 820	3	30.0	69	6	AR149416	AR149416 Sequence
821	3	30.0	70	6	AR165804	AR165804 Sequence
c 822	3	30.0	70	6	AR165804	AR165804 Sequence

823	3	30.0	70	6	AR305000	AR305000 Sequence
c 824	3	30.0	70	6	AR305000	AR305000 Sequence
825	3	30.0	71	6	AR165817	AR165817 Sequence
c 826	3	30.0	71	6	AR165817	AR165817 Sequence
827	3	30.0	71	6	AR305013	AR305013 Sequence
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829	3	30.0	71	6	AX911569	AX911569 Sequence
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831	3	30.0	71	6	BD047102	BD047102 Sequence
c 832	3	30.0	71	6	BD047102	BD047102 Sequence
833	3	30.0	72	6	AX342578	AX342578 Sequence
c 834	3	30.0	72	6	AX342578	AX342578 Sequence
835	3	30.0	72	6	AX342579	AX342579 Sequence
c 836	3	30.0	72	6	AX342579	AX342579 Sequence
837	3	30.0	73	6	AX903317	AX903317 Sequence
c 838	3	30.0	73	6	AX903317	AX903317 Sequence
839	3	30.0	73	6	AX909836	AX909836 Sequence
c 840	3	30.0	73	6	AX909836	AX909836 Sequence
841	3	30.0	73	6	BD038850	BD038850 Sequence
c 842	3	30.0	73	6	BD038850	BD038850 Sequence
843	3	30.0	73	6	BD045369	BD045369 Sequence
c 844	3	30.0	73	6	BD045369	BD045369 Sequence
845	3	30.0	77	1	BACTRNA1	D26446 Bacillus su
c 846	3	30.0	77	1	BACTRNA1	D26446 Bacillus su
847	3	30.0	81	6	AR213992	AR213992 Sequence
c 848	3	30.0	81	6	AR213992	AR213992 Sequence
849	3	30.0	81	6	AR214983	AR214983 Sequence
c 850	3	30.0	81	6	AR214983	AR214983 Sequence
851	3	30.0	81	6	AR215172	AR215172 Sequence
c 852	3	30.0	81	6	AR215172	AR215172 Sequence
853	3	30.0	81	6	AR381971	AR381971 Sequence
c 854	3	30.0	81	6	AR381971	AR381971 Sequence
855	3	30.0	81	6	AX364642	AX364642 Sequence
c 856	3	30.0	81	6	AX364642	AX364642 Sequence
857	3	30.0	81	6	AX670717	AX670717 Sequence
c 858	3	30.0	81	6	AX670717	AX670717 Sequence
859	3	30.0	82	6	AX656342	AX656342 Sequence
c 860	3	30.0	82	6	AX656342	AX656342 Sequence
861	3	30.0	82	9	AF058926	AF058926 Homo sapi
c 862	3	30.0	82	9	AF058926	AF058926 Homo sapi
863	3	30.0	84	6	AR214019	AR214019 Sequence
c 864	3	30.0	84	6	AR214019	AR214019 Sequence
865	3	30.0	84	6	AR215010	AR215010 Sequence
c 866	3	30.0	84	6	AR215010	AR215010 Sequence
867	3	30.0	84	6	AR215199	AR215199 Sequence
c 868	3	30.0	84	6	AR215199	AR215199 Sequence
869	3	30.0	84	6	AR381993	AR381993 Sequence
c 870	3	30.0	84	6	AR381993	AR381993 Sequence
871	3	30.0	84	6	AX361497	AX361497 Sequence
c 872	3	30.0	84	6	AX361497	AX361497 Sequence
873	3	30.0	84	6	AX364669	AX364669 Sequence
c 874	3	30.0	84	6	AX364669	AX364669 Sequence
875	3	30.0	84	6	AX670739	AX670739 Sequence
c 876	3	30.0	84	6	AX670739	AX670739 Sequence
877	3	30.0	84	6	AX909384	AX909384 Sequence
c 878	3	30.0	84	6	AX909384	AX909384 Sequence
879	3	30.0	84	6	BD044917	BD044917 Sequence
c 880	3	30.0	84	6	BD044917	BD044917 Sequence
881	3	30.0	85	6	AR422387	AR422387 Sequence
c 882	3	30.0	85	6	AR422387	AR422387 Sequence
883	3	30.0	85	6	AX451628	AX451628 Sequence
c 884	3	30.0	85	6	AX451628	AX451628 Sequence
885	3	30.0	85	6	AX983081	AX983081 Sequence
c 886	3	30.0	85	6	AX983081	AX983081 Sequence
887	3	30.0	85	6	BD117940	BD117940 EST and e
c 888	3	30.0	85	6	BD117940	BD117940 EST and e
889	3	30.0	87	6	AX902306	AX902306 Sequence
c 890	3	30.0	87	6	AX902306	AX902306 Sequence
891	3	30.0	87	6	BD037839	BD037839 Sequence
c 892	3	30.0	87	6	BD037839	BD037839 Sequence
893	3	30.0	90	6	BD023616	BD023616 DNA repli
c 894	3	30.0	90	6	BD023616	BD023616 DNA repli
895	3	30.0	91	6	AR216661	AR216661 Sequence
c 896	3	30.0	91	6	AR216661	AR216661 Sequence
897	3	30.0	92	6	AR059398	AR059398 Sequence
c 898	3	30.0	92	6	AR059398	AR059398 Sequence
899	3	30.0	92	6	AX902977	AX902977 Sequence
c 900	3	30.0	92	6	AX902977	AX902977 Sequence
901	3	30.0	92	6	BD038510	BD038510 Sequence
c 902	3	30.0	92	6	BD038510	BD038510 Sequence
903	3	30.0	96	6	AR173142	AR173142 Sequence
c 904	3	30.0	96	6	AR173142	AR173142 Sequence
905	3	30.0	96	6	AR173143	AR173143 Sequence
c 906	3	30.0	96	6	AR173143	AR173143 Sequence
907	3	30.0	96	6	AR173145	AR173145 Sequence
c 908	3	30.0	96	6	AR173145	AR173145 Sequence
909	3	30.0	96	8	OS09RG38R	X57909 O.sativa ra
c 910	3	30.0	96	8	OS09RG38R	X57909 O.sativa ra
911	3	30.0	96	8	SCFRRN05	M81974 Saccharum o
c 912	3	30.0	96	8	SCFRRN05	M81974 Saccharum o
913	3	30.0	96	14	EMV3APLV	M15284 Andean pota
c 914	3	30.0	96	14	EMV3APLV	M15284 Andean pota
915	3	30.0	97	6	AR165707	AR165707 Sequence
c 916	3	30.0	97	6	AR165707	AR165707 Sequence
917	3	30.0	97	6	AR304903	AR304903 Sequence
c 918	3	30.0	97	6	AR304903	AR304903 Sequence
919	3	30.0	97	6	AX914527	AX914527 Sequence
c 920	3	30.0	97	6	AX914527	AX914527 Sequence
921	3	30.0	97	6	BD050060	BD050060 Sequence
c 922	3	30.0	97	6	BD050060	BD050060 Sequence
923	3	30.0	98	6	AX904160	AX904160 Sequence
c 924	3	30.0	98	6	AX904160	AX904160 Sequence
925	3	30.0	98	6	AX918289	AX918289 Sequence
c 926	3	30.0	98	6	AX918289	AX918289 Sequence
927	3	30.0	98	6	BD039693	BD039693 Sequence
c 928	3	30.0	98	6	BD039693	BD039693 Sequence
929	3	30.0	98	6	BD053822	BD053822 Sequence
c 930	3	30.0	98	6	BD053822	BD053822 Sequence
931	3	30.0	100	6	BD270708	BD270708 Selection
c 932	3	30.0	100	6	BD270708	BD270708 Selection
933	3	30.0	100	6	AX010698	AX010698 Sequence
c 934	3	30.0	100	6	AX010698	AX010698 Sequence
935	3	30.0	100	6	AX913976	AX913976 Sequence
c 936	3	30.0	100	6	AX913976	AX913976 Sequence
937	3	30.0	100	6	BD049509	BD049509 Sequence
c 938	3	30.0	100	6	BD049509	BD049509 Sequence
939	2	20.0	5	6	CQ818363	CQ818363 Sequence
c 940	2	20.0	5	6	CQ818363	CQ818363 Sequence
941	2	20.0	5	6	AX504322	AX504322 Sequence
c 942	2	20.0	5	6	AX504322	AX504322 Sequence
943	2	20.0	5	6	AX722023	AX722023 Sequence
c 944	2	20.0	5	6	AX722023	AX722023 Sequence
945	2	20.0	6	6	BD194754	BD194754 Homogeneo
c 946	2	20.0	6	6	BD194754	BD194754 Homogeneo
947	2	20.0	6	6	BD205611	BD205611 Method of
c 948	2	20.0	6	6	BD205611	BD205611 Method of
949	2	20.0	6	6	BD261153	BD261153 Methods a
c 950	2	20.0	6	6	BD261153	BD261153 Methods a
951	2	20.0	6	6	BD261308	BD261308 Methods a
c 952	2	20.0	6	6	BD261308	BD261308 Methods a
953	2	20.0	6	6	BD267914	BD267914 Methods f
c 954	2	20.0	6	6	BD267914	BD267914 Methods f
955	2	20.0	6	6	BD270814	BD270814 Stereoiso
c 956	2	20.0	6	6	BD270814	BD270814 Stereoiso
957	2	20.0	6	6	CQ829643	CQ829643 Sequence
c 958	2	20.0	6	6	CQ829643	CQ829643 Sequence
959	2	20.0	6	6	AX105171	AX105171 Sequence
c 960	2	20.0	6	6	AX105171	AX105171 Sequence
961	2	20.0	6	6	AX235300	AX235300 Sequence
c 962	2	20.0	6	6	AX235300	AX235300 Sequence
963	2	20.0	6	6	AX376659	AX376659 Sequence
c 964	2	20.0	6	6	AX376659	AX376659 Sequence
965	2	20.0	6	6	AX412950	AX412950 Sequence
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967	2	20.0	6	6	AX557114	AX557114 Sequence
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969	2	20.0	6	6	AX711257	AX711257 Sequence
c 970	2	20.0	6	6	AX711257	AX711257 Sequence
971	2	20.0	6	6	AX786596	AX786596 Sequence
c 972	2	20.0	6	6	AX786596	AX786596 Sequence
973	2	20.0	6	6	AX933919	AX933919 Sequence
c 974	2	20.0	6	6	AX933919	AX933919 Sequence
975	2	20.0	6	6	AX933921	AX933921 Sequence
c 976	2	20.0	6	6	AX933921	AX933921 Sequence
977	2	20.0	6	6	AX933934	AX933934 Sequence
c 978	2	20.0	6	6	AX933934	AX933934 Sequence
979	2	20.0	6	6	AX933945	AX933945 Sequence
c 980	2	20.0	6	6	AX933945	AX933945 Sequence
981	2	20.0	6	6	AX933946	AX933946 Sequence
c 982	2	20.0	6	6	AX933946	AX933946 Sequence
983	2	20.0	6	6	AX933951	AX933951 Sequence
c 984	2	20.0	6	6	AX933951	AX933951 Sequence
985	2	20.0	6	6	AX933954	AX933954 Sequence
c 986	2	20.0	6	6	AX933954	AX933954 Sequence
987	2	20.0	6	6	AX933955	AX933955 Sequence
c 988	2	20.0	6	6	AX933955	AX933955 Sequence
989	2	20.0	6	6	AX933964	AX933964 Sequence
c 990	2	20.0	6	6	AX933964	AX933964 Sequence
991	2	20.0	6	6	BD069912	BD069912 Use of nu
c 992	2	20.0	6	6	BD069912	BD069912 Use of nu
993	2	20.0	6	6	BD084757	BD084757 Human ner
c 994	2	20.0	6	6	BD084757	BD084757 Human ner
995	2	20.0	7	6	BD205612	BD205612 Method of
c 996	2	20.0	7	6	BD205612	BD205612 Method of
997	2	20.0	7	6	BD261154	BD261154 Methods a
c 998	2	20.0	7	6	BD261154	BD261154 Methods a
999	2	20.0	7	6	BD261309	BD261309 Methods a
c1000	2	20.0	7	6	BD261309	BD261309 Methods a

ALIGNMENTS

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RESULT 1
A67159
LOCUS       A67159                    10 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 16 from Patent WO9741433.
ACCESSION   A67159
VERSION     A67159.1  GI:4538508
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Kouzarides,T.
  TITLE     METHOD AND MEANS FOR DISRUPTION OF p53 AND RB INTERACTION
  JOURNAL   Patent: WO 9741433-A 16 06-NOV-1997;
            CANCER RES CAMPAIGN TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 2
A67159/c
LOCUS       A67159                    10 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 16 from Patent WO9741433.
ACCESSION   A67159
VERSION     A67159.1  GI:4538508
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Kouzarides,T.
  TITLE     METHOD AND MEANS FOR DISRUPTION OF p53 AND RB INTERACTION
  JOURNAL   Patent: WO 9741433-A 16 06-NOV-1997;
            CANCER RES CAMPAIGN TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 3
AR003507
LOCUS       AR003507                  10 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5744310.
ACCESSION   AR003507
VERSION     AR003507.1  GI:3964766
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Reed,J.C.
  TITLE     Bax promoter sequence and screening assays for indentifying agents
            that regulate bax gene expression
  JOURNAL   Patent: US 5744310-A 3 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 4
AR003507/c
LOCUS       AR003507                  10 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5744310.
ACCESSION   AR003507
VERSION     AR003507.1  GI:3964766
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Reed,J.C.
  TITLE     Bax promoter sequence and screening assays for indentifying agents
            that regulate bax gene expression
  JOURNAL   Patent: US 5744310-A 3 28-APR-1998;
FEATURES             Location/Qualifiers
     source          1. .10
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                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 5
AR070749
LOCUS       AR070749                  10 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 30 from patent US 5908750.
ACCESSION   AR070749
VERSION     AR070749.1  GI:7221637
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
  TITLE     Screening assays for identifying agents that regulate the
            expression of genes involved in cell death
  JOURNAL   Patent: US 5908750-A 30 01-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 6
AR070749/c
LOCUS       AR070749                  10 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 30 from patent US 5908750.
ACCESSION   AR070749
VERSION     AR070749.1  GI:7221637
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
  TITLE     Screening assays for identifying agents that regulate the
            expression of genes involved in cell death
  JOURNAL   Patent: US 5908750-A 30 01-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 7
AR074547
LOCUS       AR074547                  10 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 3 from patent US 5955263.
ACCESSION   AR074547
VERSION     AR074547.1  GI:10001302
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Vogelstein,B., Kinzler,K.W. and Sherman,M.I.
  TITLE     Sequence specific DNA binding by p53
  JOURNAL   Patent: US 5955263-A 3 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 8
AR074547/c
LOCUS       AR074547                  10 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 3 from patent US 5955263.
ACCESSION   AR074547
VERSION     AR074547.1  GI:10001302
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Vogelstein,B., Kinzler,K.W. and Sherman,M.I.
  TITLE     Sequence specific DNA binding by p53
  JOURNAL   Patent: US 5955263-A 3 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 9
AR124219
LOCUS       AR124219                  10 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 29 from patent US 6171857.
ACCESSION   AR124219
VERSION     AR124219.1  GI:14109580
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hendrickson,E.A.
  TITLE     Leucine zipper protein, KARP-1 and methods of regulating DNA
            dependent protein kinase activity
  JOURNAL   Patent: US 6171857-A 29 09-JAN-2001;
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FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 10
AR124219/c
LOCUS       AR124219                  10 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 29 from patent US 6171857.
ACCESSION   AR124219
VERSION     AR124219.1  GI:14109580
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Hendrickson,E.A.
  TITLE     Leucine zipper protein, KARP-1 and methods of regulating DNA
            dependent protein kinase activity
  JOURNAL   Patent: US 6171857-A 29 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 11
AR157427
LOCUS       AR157427                  10 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 3 from patent US 6245515.
ACCESSION   AR157427
VERSION     AR157427.1  GI:16218366
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Vogelstein,B., Kinzler,K.W. and Sherman,M.I.
  TITLE     Sequence specific DNA binding p53
  JOURNAL   Patent: US 6245515-A 3 12-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 12
AR157427/c
LOCUS       AR157427                  10 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 3 from patent US 6245515.
ACCESSION   AR157427
VERSION     AR157427.1  GI:16218366
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Vogelstein,B., Kinzler,K.W. and Sherman,M.I.
  TITLE     Sequence specific DNA binding p53
  JOURNAL   Patent: US 6245515-A 3 12-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 13
I62424
LOCUS       I62424                    10 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 30 from patent US 5659024.
ACCESSION   I62424
VERSION     I62424.1  GI:2480372
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
  TITLE     Promotors that regulate the expression of genes involved in cell
            death
  JOURNAL   Patent: US 5659024-A 30 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 14
I62424/c
LOCUS       I62424                    10 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 30 from patent US 5659024.
ACCESSION   I62424
VERSION     I62424.1  GI:2480372
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Reed,J.C., Miyashita,T., Harigai,M. and Hanada,M.
  TITLE     Promotors that regulate the expression of genes involved in cell
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            death
  JOURNAL   Patent: US 5659024-A 30 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 15
AR303877
LOCUS       AR303877                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 24 from patent US 6544746.
ACCESSION   AR303877
VERSION     AR303877.1  GI:31692655
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Heyduk,T.
  TITLE     Rapid and sensitive proximity-based assay for the detection and
            quantification of DNA binding proteins
  JOURNAL   Patent: US 6544746-A 24 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 16
AR303877/c
LOCUS       AR303877                  10 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 24 from patent US 6544746.
ACCESSION   AR303877
VERSION     AR303877.1  GI:31692655
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Heyduk,T.
  TITLE     Rapid and sensitive proximity-based assay for the detection and
            quantification of DNA binding proteins
  JOURNAL   Patent: US 6544746-A 24 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 17
AX077262
LOCUS       AX077262                  10 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 1 from Patent WO0105421.
ACCESSION   AX077262
VERSION     AX077262.1  GI:13121849
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   de la cueva Mendez,G.C., Laskey,R.A., Mills,A.D. and diaz
            Orejas,R.C.
  TITLE     Methods employing bacterial toxin-antitoxin systems for killing
            eukaryotic cells
  JOURNAL   Patent: WO 0105421-A 1 25-JAN-2001;
            CANCER RESEARCH CAMPAIGN TECHNOLOGY LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Consensus sequence"
ORIGIN

  Query Match           100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 18
AX077262/c
LOCUS       AX077262                  10 bp    DNA     linear   PAT 22-FEB-2001
DEFINITION  Sequence 1 from Patent WO0105421.
ACCESSION   AX077262
VERSION     AX077262.1  GI:13121849
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   de la cueva Mendez,G.C., Laskey,R.A., Mills,A.D. and diaz
            Orejas,R.C.
  TITLE     Methods employing bacterial toxin-antitoxin systems for killing
            eukaryotic cells
  JOURNAL   Patent: WO 0105421-A 1 25-JAN-2001;
            CANCER RESEARCH CAMPAIGN TECHNOLOGY LIMITED (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Consensus sequence"
ORIGIN

  Query Match           100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 19
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AX339211
LOCUS       AX339211                 10 bp    DNA     linear   PAT 10-JAN-2002
DEFINITION  Sequence 5 from Patent WO0196602.
ACCESSION   AX339211
VERSION     AX339211.1  GI:18135472
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Yang,A.L. and Festing,M.
  TITLE     Methods and materials to determine the p53 status of a sample by
            determining the binding of p53 to a vector
  JOURNAL   Patent: WO 0196602-A 5 20-DEC-2001;
            MEDICAL RESEARCH COUNCIL (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Consensus sequence"
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 20
AX339211/c
LOCUS       AX339211                 10 bp    DNA     linear   PAT 10-JAN-2002
DEFINITION  Sequence 5 from Patent WO0196602.
ACCESSION   AX339211
VERSION     AX339211.1  GI:18135472
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Yang,A.L. and Festing,M.
  TITLE     Methods and materials to determine the p53 status of a sample by
            determining the binding of p53 to a vector
  JOURNAL   Patent: WO 0196602-A 5 20-DEC-2001;
            MEDICAL RESEARCH COUNCIL (GB)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Consensus sequence"
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 21
AX776278
LOCUS       AX776278                 10 bp    DNA     linear   PAT 14-JUL-2003
DEFINITION  Sequence 14 from Patent WO03048361.
ACCESSION   AX776278
VERSION     AX776278.1  GI:32693933
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hayes,I., Cotter,T., Murphy,F. and Seery,L.
  TITLE     P55pik
  JOURNAL   Patent: WO 03048361-A 14 12-JUN-2003;
            Eirx Therapeutics Ltd (IE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Mammalian p53 recognition site"
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 22
AX776278/c
LOCUS       AX776278                 10 bp    DNA     linear   PAT 14-JUL-2003
DEFINITION  Sequence 14 from Patent WO03048361.
ACCESSION   AX776278
VERSION     AX776278.1  GI:32693933
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Hayes,I., Cotter,T., Murphy,F. and Seery,L.
  TITLE     P55pik
  JOURNAL   Patent: WO 03048361-A 14 12-JUN-2003;
            Eirx Therapeutics Ltd (IE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Mammalian p53 recognition site"
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 23
AX803572
LOCUS       AX803572                 10 bp    DNA     linear   PAT 24-NOV-2003
DEFINITION  Sequence 14 from Patent WO03054010.
ACCESSION   AX803572
VERSION     AX803572.1  GI:38502146
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Hayes,I., Cotter,T., Murphy,F. and Seety,L.
  TITLE     Early stage redox-related apoptosis modulator-2 (esram-2)
  JOURNAL   Patent: WO 03054010-A 14 03-JUL-2003;
            Eirx Therapeutics Ltd (IE)
FEATURES             Location/Qualifiers
     source          1. .10
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                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="mammalian-Mammalian p53 recognition site"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 24
AX803572/c
LOCUS       AX803572                  10 bp    DNA     linear   PAT 24-NOV-2003
DEFINITION  Sequence 14 from Patent WO03054010.
ACCESSION   AX803572
VERSION     AX803572.1  GI:38502146
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Hayes,I., Cotter,T., Murphy,F. and Seety,L.
  TITLE     Early stage redox-related apoptosis modulator-2 (esram-2)
  JOURNAL   Patent: WO 03054010-A 14 03-JUL-2003;
            Eirx Therapeutics Ltd (IE)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
                     /note="mammalian-Mammalian p53 recognition site"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 25
BD064950
LOCUS       BD064950                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA.
ACCESSION   BD064950
VERSION     BD064950.1  GI:22610553
KEYWORDS    JP 2001275678-A/162.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and
            Nishikawa,K.
  TITLE     Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA
  JOURNAL   Patent: JP 2001275678-A 162 09-OCT-2001;
            SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001275678-A/162
            PD   09-OCT-2001
            PF   31-MAR-2000 JP 2000096306
            PI   TOSHIHIKO KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI
            MIMAKI,REI FUKUSHIMA,
            PI   KAZUKO NISHIKAWA
            PC   C12N15/09,C12N5/10,C12Q1/00,C12Q1/68,C12N15/00,C12N5/00 CC
            Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 26
BD064950/c
LOCUS       BD064950                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA.
ACCESSION   BD064950
VERSION     BD064950.1  GI:22610553
KEYWORDS    JP 2001275678-A/162.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Kishimoto,T., Niwa,S., Mori,Y., Sachiyo, Mimaki, Fukushima,R. and
            Nishikawa,K.
  TITLE     Method for detecting the extent of binding of transcriptional
            regulatory protein to oligoDNA
  JOURNAL   Patent: JP 2001275678-A 162 09-OCT-2001;
            SUMITOMO ELECTRIC INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001275678-A/162
            PD   09-OCT-2001
            PF   31-MAR-2000 JP 2000096306
            PI   TOSHIHIKO KISHIMOTO,SHINICHIRO NIWA,YUKO MORI,SACHIYO PI
            MIMAKI,REI FUKUSHIMA,
            PI   KAZUKO NISHIKAWA
            PC   C12N15/09,C12N5/10,C12Q1/00,C12Q1/68,C12N15/00,C12N5/00 CC
            Synthetic DNA
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 27
BD084759
LOCUS       BD084759                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human nerve growth factor exon 1 and exon 3 promoters.
ACCESSION   BD084759
VERSION     BD084759.1  GI:22630369
KEYWORDS    JP 2001521375-A/57.
```

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SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Linnik,M.D., Racke,M.M., Krakowsky,J.M. and Subramaniam,A.
  TITLE     Human nerve growth factor exon 1 and exon 3 promoters
  JOURNAL   Patent: JP 2001521375-A 57 06-NOV-2001;
            HOECHST MARION ROUSSEL INC
COMMENT     OS   Unidentified
            PN   JP 2001521375-A/57
            PD   06-NOV-2001
            PF   12-JAN-1998 JP 1998534446
            PR   06-FEB-1997 US    60/038212
            PI   MATTHEW D LINNIK,MARGARET M RACKE,JOAN M KRAKOWSKY,ARUN  PI
            SUBRAMANIAM
            PC   C07K14/48,C12Q1/68
            CC   Strandedness: Double;
            CC   Topology: Unknown;
            CC   Human nerve growth factor exon 1 and exon 3 promoters FH   Key
                      Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 28
BD084759/c
LOCUS       BD084759                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human nerve growth factor exon 1 and exon 3 promoters.
ACCESSION   BD084759
VERSION     BD084759.1  GI:22630369
KEYWORDS    JP 2001521375-A/57.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Linnik,M.D., Racke,M.M., Krakowsky,J.M. and Subramaniam,A.
  TITLE     Human nerve growth factor exon 1 and exon 3 promoters
  JOURNAL   Patent: JP 2001521375-A 57 06-NOV-2001;
            HOECHST MARION ROUSSEL INC
COMMENT     OS   Unidentified
            PN   JP 2001521375-A/57
            PD   06-NOV-2001
            PF   12-JAN-1998 JP 1998534446
            PR   06-FEB-1997 US    60/038212
            PI   MATTHEW D LINNIK,MARGARET M RACKE,JOAN M KRAKOWSKY,ARUN  PI
            SUBRAMANIAM
            PC   C07K14/48,C12Q1/68
            CC   Strandedness: Double;
            CC   Topology: Unknown;
            CC   Human nerve growth factor exon 1 and exon 3 promoters FH   Key
                      Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 29
AX685336
LOCUS       AX685336                  19 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 26 from Patent WO02064790.
ACCESSION   AX685336
VERSION     AX685336.1  GI:29371660
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yu,J., Kinzler,K.W. and Vogelstein,B.
  TITLE     Jfy1 protein induces rapid apoptosis
  JOURNAL   Patent: WO 02064790-A 26 22-AUG-2002;
            The Johns Hopkins University (US)
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 19


RESULT 30
AX685336/c
LOCUS       AX685336                  19 bp    DNA     linear   PAT 29-MAR-2003
DEFINITION  Sequence 26 from Patent WO02064790.
ACCESSION   AX685336
VERSION     AX685336.1  GI:29371660
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yu,J., Kinzler,K.W. and Vogelstein,B.
  TITLE     Jfy1 protein induces rapid apoptosis
  JOURNAL   Patent: WO 02064790-A 26 22-AUG-2002;
            The Johns Hopkins University (US)
FEATURES              Location/Qualifiers
     source           1. .19
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 10;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         19 RRRCWWGYYY 10
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RESULT 31
AR181179
LOCUS       AR181179                  20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 6 from patent US 6335156.
ACCESSION   AR181179
VERSION     AR181179.1  GI:20223393
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hermeking,H., Vogelstein,B. and Kinzler,K.W.
  TITLE     14-3-3.sigma. arrests the cell cycle
  JOURNAL   Patent: US 6335156-A 6 01-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 32
AR181179/c
LOCUS       AR181179                  20 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 6 from patent US 6335156.
ACCESSION   AR181179
VERSION     AR181179.1  GI:20223393
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hermeking,H., Vogelstein,B. and Kinzler,K.W.
  TITLE     14-3-3.sigma. arrests the cell cycle
  JOURNAL   Patent: US 6335156-A 6 01-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         20 RRRCWWGYYY 11


RESULT 33
AR060431
LOCUS       AR060431                  21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5840673.
ACCESSION   AR060431
VERSION     AR060431.1  GI:5986881
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Buckbinder,L.R., Kley,N. and Seizinger,B.R.
  TITLE     Insulin-like growth factor binding protein 3 (IGF-BP3) in treatment
            of p53-related tumors
  JOURNAL   Patent: US 5840673-A 4 24-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 34
AR060431/c
LOCUS       AR060431                  21 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5840673.
ACCESSION   AR060431
VERSION     AR060431.1  GI:5986881
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Buckbinder,L.R., Kley,N. and Seizinger,B.R.
  TITLE     Insulin-like growth factor binding protein 3 (IGF-BP3) in treatment
            of p53-related tumors
  JOURNAL   Patent: US 5840673-A 4 24-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            100.0%;  Score 10;  DB 6;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         21 RRRCWWGYYY 12


RESULT 35
I22646
LOCUS       I22646                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 134 from patent US 5527898.
ACCESSION   I22646
VERSION     I22646.1  GI:1603000
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
            Resnick,R.M. and Zhang,T.Y.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5527898-A 134 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            50.0%;  Score 5;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWGYY 9
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```
Db         11 WWGYY 15


RESULT 36
I22646/c
LOCUS       I22646                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 134 from patent US 5527898.
ACCESSION   I22646
VERSION     I22646.1  GI:1603000
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
            Resnick,R.M. and Zhang,T.Y.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5527898-A 134 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             50.0%;  Score 5;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRCWW 6
              |||||
Db         15 RRCWW 11


RESULT 37
I47471
LOCUS       I47471                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 134 from patent US 5639871.
ACCESSION   I47471
VERSION     I47471.1  GI:2471436
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Impraim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5639871-A 134 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             50.0%;  Score 5;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWGYY 9
              |||||
Db         11 WWGYY 15


RESULT 38
I47471/c
LOCUS       I47471                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 134 from patent US 5639871.
ACCESSION   I47471
VERSION     I47471.1  GI:2471436
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Impraim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5639871-A 134 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             50.0%;  Score 5;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRCWW 6
              |||||
Db         15 RRCWW 11


RESULT 39
CQ771564
LOCUS       CQ771564                  10 bp    DNA     linear   PAT 04-MAR-2004
DEFINITION  Sequence 1 from Patent EP1138781.
ACCESSION   CQ771564
VERSION     CQ771564.1  GI:45125554
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kulesz-Martin,M.F. and Liu,Y.
  TITLE     Method for Quantifying DNA binding activity of DNA binding proteins
  JOURNAL   Patent: EP 1138781-A 1 04-OCT-2001;
            HEALTH RESEARCH, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Specific to p53 protein; p53 consensus sequence"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db          1 RRRC 4


RESULT 40
CQ771564/c
LOCUS       CQ771564                  10 bp    DNA     linear   PAT 04-MAR-2004
DEFINITION  Sequence 1 from Patent EP1138781.
ACCESSION   CQ771564
VERSION     CQ771564.1  GI:45125554
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Kulesz-Martin,M.F. and Liu,Y.
  TITLE     Method for Quantifying DNA binding activity of DNA binding proteins
  JOURNAL   Patent: EP 1138781-A 1 04-OCT-2001;
            HEALTH RESEARCH, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Specific to p53 protein; p53 consensus sequence"
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ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         10 RRRC 7


RESULT 41
I74680
LOCUS       I74680                    10 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 9 from patent US 5688918.
ACCESSION   I74680
VERSION     I74680.1  GI:3010821
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Kulesz-Martin,M.F.
  TITLE     p53as protein and antibody therefor
  JOURNAL   Patent: US 5688918-A 9 18-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db          4 CWWG 7


RESULT 42
I74680/c
LOCUS       I74680                    10 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 9 from patent US 5688918.
ACCESSION   I74680
VERSION     I74680.1  GI:3010821
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Kulesz-Martin,M.F.
  TITLE     p53as protein and antibody therefor
  JOURNAL   Patent: US 5688918-A 9 18-NOV-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db          7 CWWG 4


RESULT 43
I91766
LOCUS       I91766                    10 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 9 from patent US 5726024.
ACCESSION   I91766
VERSION     I91766.1  GI:3936236
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Kulesz-Martin,M.F.
  TITLE     p53as protein and antibody therefor
  JOURNAL   Patent: US 5726024-A 9 10-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db          4 CWWG 7


RESULT 44
I91766/c
LOCUS       I91766                    10 bp    DNA     linear   PAT 01-DEC-1998
DEFINITION  Sequence 9 from patent US 5726024.
ACCESSION   I91766
VERSION     I91766.1  GI:3936236
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Kulesz-Martin,M.F.
  TITLE     p53as protein and antibody therefor
  JOURNAL   Patent: US 5726024-A 9 10-MAR-1998;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db          7 CWWG 4


RESULT 45
BD090936
LOCUS       BD090936                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for quantifying DNA binding activity of DNA binding
            proteins.
ACCESSION   BD090936
VERSION     BD090936.1  GI:22636546
KEYWORDS    JP 2001321199-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Martin,M.F.K. and Liu,Y.
  TITLE     Method for quantifying DNA binding activity of DNA binding proteins
  JOURNAL   Patent: JP 2001321199-A 1 20-NOV-2001;
            HEALTH RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001321199-A/1
            PD   20-NOV-2001
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            PF   02-APR-2001 JP 2001103067
            PR   31-MAR-2000 US    09/539945
            PI   MOLLY F KULESZ MARTIN,YUANGANG LIU
            PC   C12Q1/68,C07K14/47,C12N15/09,G01N33/15,G01N33/50,G01N33/53, PC
              G01N33/566//
            PC   C12M1/00,C12M1/20,C12M1/34,C12N15/00
            CC   Method for quantifying DNA binding activity of DNA binding  CC
                   proteins
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match            40.0%;  Score 4;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db          1 RRRC 4


RESULT 46
BD090936/c
LOCUS       BD090936                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Method for quantifying DNA binding activity of DNA binding
            proteins.
ACCESSION   BD090936
VERSION     BD090936.1  GI:22636546
KEYWORDS    JP 2001321199-A/1.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Martin,M.F.K. and Liu,Y.
  TITLE     Method for quantifying DNA binding activity of DNA binding proteins
  JOURNAL   Patent: JP 2001321199-A 1 20-NOV-2001;
            HEALTH RESEARCH INC
COMMENT     OS   Artificial Sequence
            PN   JP 2001321199-A/1
            PD   20-NOV-2001
            PF   02-APR-2001 JP 2001103067
            PR   31-MAR-2000 US    09/539945
            PI   MOLLY F KULESZ MARTIN,YUANGANG LIU
            PC   C12Q1/68,C07K14/47,C12N15/09,G01N33/15,G01N33/50,G01N33/53, PC
              G01N33/566//
            PC   C12M1/00,C12M1/20,C12M1/34,C12N15/00
            CC   Method for quantifying DNA binding activity of DNA binding  CC
                   proteins
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match            40.0%;  Score 4;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         10 RRRC 7


RESULT 47
BD084901
LOCUS       BD084901                  12 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterising DNA.
ACCESSION   BD084901
VERSION     BD084901.1  GI:22630511
KEYWORDS    JP 2001521398-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Schmidt,G. and Thompson,A.H.
  TITLE     Characterising DNA
  JOURNAL   Patent: JP 2001521398-A 7 06-NOV-2001;
            BRAX GROUP LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001521398-A/7
            PD   06-NOV-2001
            PF   20-APR-1998 JP 1998545274
            PR   21-APR-1997 GB    9707980.0
            PI   GUNTER SCHMIDT,ANDREW HUGIN THOMPSON
            PC   C12Q1/68
            CC   Adapter oligonucleotide comprising a recognition site for a
            CC           sampling
            CC   cleavage agent
            FH   Key             Location/Qualifiers
            FT   unsure          (1). .(12).
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match            40.0%;  Score 4;  DB 6;  Length 12;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db          8 GYYY 11


RESULT 48
BD084901/c
LOCUS       BD084901                  12 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Characterising DNA.
ACCESSION   BD084901
VERSION     BD084901.1  GI:22630511
KEYWORDS    JP 2001521398-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Schmidt,G. and Thompson,A.H.
  TITLE     Characterising DNA
  JOURNAL   Patent: JP 2001521398-A 7 06-NOV-2001;
            BRAX GROUP LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001521398-A/7
            PD   06-NOV-2001
            PF   20-APR-1998 JP 1998545274
            PR   21-APR-1997 GB    9707980.0
            PI   GUNTER SCHMIDT,ANDREW HUGIN THOMPSON
            PC   C12Q1/68
            CC   Adapter oligonucleotide comprising a recognition site for a
            CC           sampling
            CC   cleavage agent
            FH   Key             Location/Qualifiers
            FT   unsure          (1). .(12).
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         11 RRRC 8


RESULT 49
AR451567
LOCUS       AR451567                  19 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 212 from patent US 6673917.
ACCESSION   AR451567
VERSION     AR451567.1  GI:42682592
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Korneluk,R.G., LaCasse,E., Baird,S., Holcik,M. and Young,S.
  TITLE     Antisense IAP nucleic acids and uses thereof
  JOURNAL   Patent: US 6673917-A 212 06-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         16 GYYY 19


RESULT 50
AR451567/c
LOCUS       AR451567                  19 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 212 from patent US 6673917.
ACCESSION   AR451567
VERSION     AR451567.1  GI:42682592
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Korneluk,R.G., LaCasse,E., Baird,S., Holcik,M. and Young,S.
  TITLE     Antisense IAP nucleic acids and uses thereof
  JOURNAL   Patent: US 6673917-A 212 06-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         19 RRRC 16


RESULT 51
AX412112
LOCUS       AX412112                  19 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 212 from Patent WO0226968.
ACCESSION   AX412112
VERSION     AX412112.1  GI:21444577
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
  TITLE     Antisense iap nucleic acids and uses thereof
  JOURNAL   Patent: WO 0226968-A 212 04-APR-2002;
            University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         16 GYYY 19


RESULT 52
AX412112/c
LOCUS       AX412112                  19 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 212 from Patent WO0226968.
ACCESSION   AX412112
VERSION     AX412112.1  GI:21444577
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
  TITLE     Antisense iap nucleic acids and uses thereof
  JOURNAL   Patent: WO 0226968-A 212 04-APR-2002;
            University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         19 RRRC 16


RESULT 53
BD184677
LOCUS       BD184677                  20 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Method and detector for identifying subtypes of human papiloma
            viruses.
ACCESSION   BD184677
VERSION     BD184677.1  GI:31876877
KEYWORDS    JP 2002360271-A/656.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
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            Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
  TITLE     Method and detector for identifying subtypes of human papiloma
  JOURNAL   Patent: JP 2002360271-A 656 17-DEC-2002;
            KING CAR FOOD INDUSTRIAL CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002360271-A/656
            PD   17-DEC-2002
            PF   28-NOV-2001 JP 2001362595
            PR   04-MAY-2001 TW     90110785
            PI   CHING-YEE LING,RUEY-WEN LIN,ZHOU-MENG YOO,XIN-HSUAN HUANG,BOW-
            PI   HAENG LEE,
            PI   SHENG-HSIUNG LEE,YI-JU LIN,CI-CHUNG HUANG,HAN-CHANG HSU,CHA-
            PI   WEN SHI,
            PI   CHIH-XIN YEH,YI-FENG CAO,CHIH-LONG PAN
            PC   C12N15/09,C12N15/09,C12M1/34,C12Q1/04,C12Q1/42,C12Q1/68 PC
            ,C12Q1/70,G01N21/64,
            PC   G01N33/53,G01N33/574,G01N33/58,G01N37/00//(C12M1/34,C12R1:93),
            PC   (C12Q1/70,C12R1:93),C12N15/00,C12N15/00
            CC   E1 350L primer.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db          6 GYYY 9


RESULT 54
BD184677/c
LOCUS       BD184677                  20 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Method and detector for identifying subtypes of human papiloma
            viruses.
ACCESSION   BD184677
VERSION     BD184677.1  GI:31876877
KEYWORDS    JP 2002360271-A/656.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
            Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
  TITLE     Method and detector for identifying subtypes of human papiloma
  JOURNAL   Patent: JP 2002360271-A 656 17-DEC-2002;
            KING CAR FOOD INDUSTRIAL CO LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2002360271-A/656
            PD   17-DEC-2002
            PF   28-NOV-2001 JP 2001362595
            PR   04-MAY-2001 TW     90110785
            PI   CHING-YEE LING,RUEY-WEN LIN,ZHOU-MENG YOO,XIN-HSUAN HUANG,BOW-
            PI   HAENG LEE,
            PI   SHENG-HSIUNG LEE,YI-JU LIN,CI-CHUNG HUANG,HAN-CHANG HSU,CHA-
            PI   WEN SHI,
            PI   CHIH-XIN YEH,YI-FENG CAO,CHIH-LONG PAN
            PC   C12N15/09,C12N15/09,C12M1/34,C12Q1/04,C12Q1/42,C12Q1/68 PC
            ,C12Q1/70,G01N21/64,
            PC   G01N33/53,G01N33/574,G01N33/58,G01N37/00//(C12M1/34,C12R1:93),
            PC   (C12Q1/70,C12R1:93),C12N15/00,C12N15/00
            CC   E1 350L primer.
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db          9 RRRC 6


RESULT 55
I22645
LOCUS       I22645                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 133 from patent US 5527898.
ACCESSION   I22645
VERSION     I22645.1  GI:1602999
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
            Resnick,R.M. and Zhang,T.Y.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5527898-A 133 18-JUN-1996;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWGY 8
              ||||
Db         11 WWGY 14


RESULT 56
I22645/c
LOCUS       I22645                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 133 from patent US 5527898.
ACCESSION   I22645
VERSION     I22645.1  GI:1602999
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
            Resnick,R.M. and Zhang,T.Y.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5527898-A 133 18-JUN-1996;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RCWW 6
              ||||
```

```
Db         14 RCWW 11


RESULT 57
I22647
LOCUS       I22647                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 135 from patent US 5527898.
ACCESSION   I22647
VERSION     I22647.1  GI:1603001
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
            Resnick,R.M. and Zhang,T.Y.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5527898-A 135 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WGYY 9
              ||||
Db         12 WGYY 15


RESULT 58
I22647/c
LOCUS       I22647                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 135 from patent US 5527898.
ACCESSION   I22647
VERSION     I22647.1  GI:1603001
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Manos,M.Michele.,
            Resnick,R.M. and Zhang,T.Y.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5527898-A 135 18-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRCW 5
              ||||
Db         15 RRCW 12


RESULT 59
I47470
LOCUS       I47470                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 133 from patent US 5639871.
ACCESSION   I47470
VERSION     I47470.1  GI:2471435
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Impraim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5639871-A 133 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWGY 8
              ||||
Db         11 WWGY 14


RESULT 60
I47470/c
LOCUS       I47470                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 133 from patent US 5639871.
ACCESSION   I47470
VERSION     I47470.1  GI:2471435
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Impraim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5639871-A 133 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RCWW 6
              ||||
Db         14 RCWW 11


RESULT 61
I47472
LOCUS       I47472                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 135 from patent US 5639871.
ACCESSION   I47472
VERSION     I47472.1  GI:2471437
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Impraim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5639871-A 135 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
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  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WGYY 9
              ||||
Db         12 WGYY 15


RESULT 62
I47472/c
LOCUS       I47472                  20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 135 from patent US 5639871.
ACCESSION   I47472
VERSION     I47472.1  GI:2471437
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bauer,H.M., Gravitt,P.E., Greer,C.E., Impraim,C.C.,
            Manos,M.Michele., Resnick,R.M. and Zhang,T.Yi.
  TITLE     Detection of human papillomavirus by the polymerase chain reaction
  JOURNAL   Patent: US 5639871-A 135 17-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRCW 5
              ||||
Db         15 RRCW 12


RESULT 63
AR030183
LOCUS       AR030183                27 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 7 from patent US 5861245.
ACCESSION   AR030183
VERSION     AR030183.1  GI:5943397
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.Thomas. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 5861245-A 7 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         15 RRRC 18


RESULT 64
AR030183/c
LOCUS       AR030183                27 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 7 from patent US 5861245.
ACCESSION   AR030183
VERSION     AR030183.1  GI:5943397
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.Thomas. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 5861245-A 7 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         18 GYYY 15


RESULT 65
AR030187
LOCUS       AR030187                27 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 11 from patent US 5861245.
ACCESSION   AR030187
VERSION     AR030187.1  GI:5943401
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.Thomas. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 5861245-A 11 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         15 RRRC 18


RESULT 66
AR030187/c
LOCUS       AR030187                27 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 11 from patent US 5861245.
ACCESSION   AR030187
VERSION     AR030187.1  GI:5943401
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.Thomas. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 5861245-A 11 19-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         18 GYYY 15


RESULT 67
AR140600
LOCUS       AR140600                  27 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 7 from patent US 6207810.
ACCESSION   AR140600
VERSION     AR140600.1  GI:14483096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M. and Welsh,J.T.
  TITLE     TRT1 polynucleotides, host cells and assays
  JOURNAL   Patent: US 6207810-A 7 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         15 RRRC 18


RESULT 68
AR140600/c
LOCUS       AR140600                  27 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 7 from patent US 6207810.
ACCESSION   AR140600
VERSION     AR140600.1  GI:14483096
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M. and Welsh,J.T.
  TITLE     TRT1 polynucleotides, host cells and assays
  JOURNAL   Patent: US 6207810-A 7 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         18 GYYY 15


RESULT 69
I17358
LOCUS       I17358                    27 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 8 from patent US 5487985.
ACCESSION   I17358
VERSION     I17358.1  GI:1252266
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.T. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 5487985-A 8 30-JAN-1996;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         15 RRRC 18


RESULT 70
I17358/c
LOCUS       I17358                    27 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 8 from patent US 5487985.
ACCESSION   I17358
VERSION     I17358.1  GI:1252266
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.T. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 5487985-A 8 30-JAN-1996;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         18 GYYY 15


RESULT 71
I17359
LOCUS       I17359                    27 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 9 from patent US 5487985.
ACCESSION   I17359
VERSION     I17359.1  GI:1252267
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.T. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 5487985-A 9 30-JAN-1996;
FEATURES             Location/Qualifiers
     source          1. .27
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                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         15 RRRC 18


RESULT 72
I17359/c
LOCUS       I17359                    27 bp    DNA     linear   PAT 03-APR-1996
DEFINITION  Sequence 9 from patent US 5487985.
ACCESSION   I17359
VERSION     I17359.1  GI:1252267
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.T. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 5487985-A 9 30-JAN-1996;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         18 GYYY 15


RESULT 73
AR477281
LOCUS       AR477281                  27 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 8 from patent US 6696277.
ACCESSION   AR477281
VERSION     AR477281.1  GI:47234616
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.T. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 6696277-A 8 24-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         15 RRRC 18


RESULT 74
AR477281/c
LOCUS       AR477281                  27 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 8 from patent US 6696277.
ACCESSION   AR477281
VERSION     AR477281.1  GI:47234616
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.T. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 6696277-A 8 24-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         18 GYYY 15


RESULT 75
AR477282
LOCUS       AR477282                  27 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 9 from patent US 6696277.
ACCESSION   AR477282
VERSION     AR477282.1  GI:47234617
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.T. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
            fingerprinting genomes
  JOURNAL   Patent: US 6696277-A 9 24-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         15 RRRC 18


RESULT 76
AR477282/c
LOCUS       AR477282                  27 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 9 from patent US 6696277.
ACCESSION   AR477282
VERSION     AR477282.1  GI:47234617
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   McClelland,M., Welsh,J.T. and Sorge,J.A.
  TITLE     Arbitrarily primed polymerase chain reaction method for
```

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            fingerprinting genomes
  JOURNAL   Patent: US 6696277-A 9 24-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         18 GYYY 15


RESULT 77
BD132388
LOCUS       BD132388                  38 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  DNA diagnosis method based on mass spectrometry.
ACCESSION   BD132388
VERSION     BD132388.1  GI:23227333
KEYWORDS    JP 2002507883-A/320.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
            Boom,D.V.D., Jurinke,C. and Rupert,A.
  TITLE     DNA diagnosis method based on mass spectrometry
  JOURNAL   Patent: JP 2002507883-A 320 12-MAR-2002;
            SEQUENOM INC
COMMENT     PN   JP 2002507883-A/320
            PD   12-MAR-2002
            PF   06-NOV-1997 JP 1998521832
            PR   06-NOV-1996 US    08/744481,06-NOV-1996 US    08/746036 PR
            06-NOV-1996 US    08/746055,06-NOV-1996 US    08/744590 PR
            23-JAN-1997 US    08/786988,23-JAN-1997 US    08/787639 PR
            19-SEP-1997 US    08/933792,08-OCT-1997 US    08/947801 PI   HUBERT
            KOSTER,DANIEL P LITTLE,ANDREAS BRAUN,DAVID M LOUGH, PI   GUOBING
            XIANG,
            PI   DIRK VAN DEN BOOM,CHRISTIAN JURINKE,ANDREAS RUPERT PC
            C12Q1/68,C07H21/00,C07F9/24
            CC   Strandedness: Single;
            CC   Topology: Unknown;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db         33 CWWG 36


RESULT 78
BD132388/c
LOCUS       BD132388                  38 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  DNA diagnosis method based on mass spectrometry.
ACCESSION   BD132388
VERSION     BD132388.1  GI:23227333
KEYWORDS    JP 2002507883-A/320.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,
            Boom,D.V.D., Jurinke,C. and Rupert,A.
  TITLE     DNA diagnosis method based on mass spectrometry
  JOURNAL   Patent: JP 2002507883-A 320 12-MAR-2002;
            SEQUENOM INC
COMMENT     PN   JP 2002507883-A/320
            PD   12-MAR-2002
            PF   06-NOV-1997 JP 1998521832
            PR   06-NOV-1996 US    08/744481,06-NOV-1996 US    08/746036 PR
            06-NOV-1996 US    08/746055,06-NOV-1996 US    08/744590 PR
            23-JAN-1997 US    08/786988,23-JAN-1997 US    08/787639 PR
            19-SEP-1997 US    08/933792,08-OCT-1997 US    08/947801 PI   HUBERT
            KOSTER,DANIEL P LITTLE,ANDREAS BRAUN,DAVID M LOUGH, PI   GUOBING
            XIANG,
            PI   DIRK VAN DEN BOOM,CHRISTIAN JURINKE,ANDREAS RUPERT PC
            C12Q1/68,C07H21/00,C07F9/24
            CC   Strandedness: Single;
            CC   Topology: Unknown;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db         36 CWWG 33


RESULT 79
AX328823
LOCUS       AX328823                  42 bp    DNA     linear   PAT 08-JAN-2002
DEFINITION  Sequence 320 from Patent EP1164203.
ACCESSION   AX328823
VERSION     AX328823.1  GI:18102022
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
            Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
  TITLE     Dna diagnostics based on mass spectrometry
  JOURNAL   Patent: EP 1164203-A 320 19-DEC-2001;
            SEQUENOM, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db         33 CWWG 36


RESULT 80
AX328823/c
LOCUS       AX328823                  42 bp    DNA     linear   PAT 08-JAN-2002
DEFINITION  Sequence 320 from Patent EP1164203.
ACCESSION   AX328823
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```
VERSION     AX328823.1  GI:18102022
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Koester,H., Little,D.P., Braun,A., Jurinke,C., van den Boom,D.,
            Xiang,G., Lough,D.M., Ruppert,A. and Hillenkamp,F.
  TITLE     Dna diagnostics based on mass spectrometry
  JOURNAL   Patent: EP 1164203-A 320 19-DEC-2001;
            SEQUENOM, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .42
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 6;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db         36 CWWG 33


RESULT 81
DOGSR7SL1
LOCUS       DOGSR7SL1                63 bp ss-RNA     linear   MAM 27-APR-1993
DEFINITION  Dog signal recognition particle 7SL RNA, 5' end.
ACCESSION   M30845
VERSION     M30845.1  GI:174286
KEYWORDS    7SL RNA.
SEGMENT     1 of 2
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   Gundelfinger,E.D., Krause,E., Melli,M. and Dobberstein,B.
  TITLE     The organization of the 7SL RNA in the signal recognition particle
  JOURNAL   Nucleic Acids Res. 11 (21), 7363-7374 (1983)
  MEDLINE   84069772
   PUBMED   6196719
COMMENT     Original source text: Canis sp. pancreas scRNA.
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Canis sp."
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9616"
                     /tissue_type="pancreas"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 4;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db          8 GYYY 11


RESULT 82
DOGSR7SL1/c
LOCUS       DOGSR7SL1                63 bp ss-RNA     linear   MAM 27-APR-1993
DEFINITION  Dog signal recognition particle 7SL RNA, 5' end.
ACCESSION   M30845
VERSION     M30845.1  GI:174286
KEYWORDS    7SL RNA.
SEGMENT     1 of 2
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   Gundelfinger,E.D., Krause,E., Melli,M. and Dobberstein,B.
  TITLE     The organization of the 7SL RNA in the signal recognition particle
  JOURNAL   Nucleic Acids Res. 11 (21), 7363-7374 (1983)
  MEDLINE   84069772
   PUBMED   6196719
COMMENT     Original source text: Canis sp. pancreas scRNA.
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Canis sp."
                     /mol_type="genomic RNA"
                     /db_xref="taxon:9616"
                     /tissue_type="pancreas"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 4;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         59 RRRC 56


RESULT 83
A90866
LOCUS       A90866                   6 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1 from Patent EP0855184.
ACCESSION   A90866
VERSION     A90866.1  GI:6739260
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 1 29-JUL-1998;
            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          1 RRC 3


RESULT 84
A90866/c
LOCUS       A90866                   6 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1 from Patent EP0855184.
ACCESSION   A90866
VERSION     A90866.1  GI:6739260
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Heeg,K.P. and Lipford,G.B.
  TITLE     Pharmaceutical composition comprising a polynucleotide and an
            antigen especially for vaccination
  JOURNAL   Patent: EP 0855184-A 1 29-JUL-1998;
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            HEEG KLAUS PROF DR (DE); LIPFORD GRAYSON B DR (DE)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYY 9
              |||
Db          3 GYY 1


RESULT 85
E64767
LOCUS       E64767                     6 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Chemically synthesized artificial promoter for realizing high-level
            expression of introduced gene and method for synthesizing the
            same.
ACCESSION   E64767
VERSION     E64767.1  GI:18628530
KEYWORDS    JP 2000139477-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Tori,R., Sawanto,S.B., Synge,P.K. and Guputa,S.K.
  TITLE     Chemically synthesized artificial promoter for realizing high-level
            expression of introduced gene and method for synthesizing the same
  JOURNAL   Patent: JP 2000139477-A 8 23-MAY-2000;
            COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2000139477-A/8
            PD   23-MAY-2000
            PF   27-APR-1999 JP 1999119227
            PR   09-NOV-1998 IN      3322/98
            PI   RAKESH TORI,SALLY BISHUWANATO SAWANTO,PURAJUNNA KUMAR SYNGE,
            PI   SHIFU KUMAR GUPUTA
            PC   C12N15/09,C12N5/10,C12N15/00,C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .6
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          1 CWW 3


RESULT 86
E64767/c
LOCUS       E64767                     6 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Chemically synthesized artificial promoter for realizing high-level
            expression of introduced gene and method for synthesizing the
            same.
ACCESSION   E64767
VERSION     E64767.1  GI:18628530
KEYWORDS    JP 2000139477-A/8.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 6)
  AUTHORS   Tori,R., Sawanto,S.B., Synge,P.K. and Guputa,S.K.
  TITLE     Chemically synthesized artificial promoter for realizing high-level
            expression of introduced gene and method for synthesizing the same
  JOURNAL   Patent: JP 2000139477-A 8 23-MAY-2000;
            COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2000139477-A/8
            PD   23-MAY-2000
            PF   27-APR-1999 JP 1999119227
            PR   09-NOV-1998 IN      3322/98
            PI   RAKESH TORI,SALLY BISHUWANATO SAWANTO,PURAJUNNA KUMAR SYNGE,
            PI   SHIFU KUMAR GUPUTA
            PC   C12N15/09,C12N5/10,C12N15/00,C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .6
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          6 WWG 4


RESULT 87
AX797664
LOCUS       AX797664                   6 bp    DNA     linear   PAT 08-OCT-2003
DEFINITION  Sequence 27 from Patent WO03039595.
ACCESSION   AX797664
VERSION     AX797664.1  GI:37518092
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Semple,S., Klimuk,S. and Yuan,Z.N.
  TITLE     Mucosal adjuvants comprising an oligonucleotide and a cationic
            lipid
  JOURNAL   Patent: WO 03039595-A 27 15-MAY-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          1 RRC 3


RESULT 88
AX797664/c
LOCUS       AX797664                   6 bp    DNA     linear   PAT 08-OCT-2003
DEFINITION  Sequence 27 from Patent WO03039595.
ACCESSION   AX797664
```

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VERSION     AX797664.1  GI:37518092
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Semple,S., Klimuk,S. and Yuan,Z.N.
  TITLE     Mucosal adjuvants comprising an oligonucleotide and a cationic
            lipid
  JOURNAL   Patent: WO 03039595-A 27 15-MAY-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          6 RRC 4


RESULT 89
AX957648
LOCUS       AX957648                  6 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 27 from Patent WO03094963.
ACCESSION   AX957648
VERSION     AX957648.1  GI:40785520
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.
  TITLE     Methylated immunostimulatory oligonucleotides and methods of using
            the same
  JOURNAL   Patent: WO 03094963-A 27 20-NOV-2003;
            Inex Pharmaceuticals Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          1 RRC 3


RESULT 90
AX957648/c
LOCUS       AX957648                  6 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 27 from Patent WO03094963.
ACCESSION   AX957648
VERSION     AX957648.1  GI:40785520
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.
  TITLE     Methylated immunostimulatory oligonucleotides and methods of using
            the same
  JOURNAL   Patent: WO 03094963-A 27 20-NOV-2003;
            Inex Pharmaceuticals Corporation (CA)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          6 RRC 4


RESULT 91
AX957742
LOCUS       AX957742                  6 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 27 from Patent WO03094828.
ACCESSION   AX957742
VERSION     AX957742.1  GI:40785560
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.
  TITLE     Cancer vaccines and methods of using the same
  JOURNAL   Patent: WO 03094828-A 27 20-NOV-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          1 RRC 3


RESULT 92
AX957742/c
LOCUS       AX957742                  6 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 27 from Patent WO03094828.
ACCESSION   AX957742
VERSION     AX957742.1  GI:40785560
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Tam,Y.K., Semple,S., Klimuk,S. and Chikh,G.
  TITLE     Cancer vaccines and methods of using the same
  JOURNAL   Patent: WO 03094828-A 27 20-NOV-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"
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ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          6 RRC 4


RESULT 93
AX958147
LOCUS       AX958147                  6 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 27 from Patent WO03094829.
ACCESSION   AX958147
VERSION     AX958147.1  GI:40785811
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Semple,S., Chikh,G., Hope,M.J. and Tam,Y.K.
  TITLE     Pathogen vaccines and methods for using the same
  JOURNAL   Patent: WO 03094829-A 27 20-NOV-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          1 RRC 3


RESULT 94
AX958147/c
LOCUS       AX958147                  6 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 27 from Patent WO03094829.
ACCESSION   AX958147
VERSION     AX958147.1  GI:40785811
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Semple,S., Chikh,G., Hope,M.J. and Tam,Y.K.
  TITLE     Pathogen vaccines and methods for using the same
  JOURNAL   Patent: WO 03094829-A 27 20-NOV-2003;
            Inex Pharmaceuticals Corp. (CA)
FEATURES             Location/Qualifiers
     source          1. .6
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          6 RRC 4


RESULT 95
BD211369
LOCUS       BD211369                  7 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of finding restriction enzyme.
ACCESSION   BD211369
VERSION     BD211369.1  GI:33021139
KEYWORDS    JP 2002517260-A/93.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 7)
  AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
  TITLE     Method of finding restriction enzyme
  JOURNAL   Patent: JP 2002517260-A 93 18-JUN-2002;
            NEW ENGLAND BIOLABS INC
COMMENT     OS   Unknown
            PN   JP 2002517260-A/93
            PD   18-JUN-2002
            PF   11-JUN-1999 JP 2000553622
            PR   12-JUN-1998 US    60/089086,12-JUN-1998 US    60/089101 PI
            ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
            C12Q1/68,C12N15/09,C12N15/00
            CC   Description of Unknown Organism: Consensus sequence CC
            Position 4, 5 & 6 - R = A or G; Position 7 - Y = C or T FH   Key
                     Location/Qualifiers
            FT   source          1. .7
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
     source          1. .7
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          4 RRR 6


RESULT 96
BD211369/c
LOCUS       BD211369                  7 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of finding restriction enzyme.
ACCESSION   BD211369
VERSION     BD211369.1  GI:33021139
KEYWORDS    JP 2002517260-A/93.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 7)
  AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
  TITLE     Method of finding restriction enzyme
  JOURNAL   Patent: JP 2002517260-A 93 18-JUN-2002;
            NEW ENGLAND BIOLABS INC
COMMENT     OS   Unknown
            PN   JP 2002517260-A/93
            PD   18-JUN-2002
            PF   11-JUN-1999 JP 2000553622
            PR   12-JUN-1998 US    60/089086,12-JUN-1998 US    60/089101 PI
            ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
            C12Q1/68,C12N15/09,C12N15/00
            CC   Description of Unknown Organism: Consensus sequence CC
            Position 4, 5 & 6 - R = A or G; Position 7 - Y = C or T FH   Key
                     Location/Qualifiers
            FT   source          1. .7
            FT                   /organism='Unknown'.
FEATURES             Location/Qualifiers
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     source          1. .7
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          6 YYY 4


RESULT 97
BD211370
LOCUS       BD211370                  7 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of finding restriction enzyme.
ACCESSION   BD211370
VERSION     BD211370.1  GI:33021140
KEYWORDS    JP 2002517260-A/94.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 7)
  AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
  TITLE     Method of finding restriction enzyme
  JOURNAL   Patent: JP 2002517260-A 94 18-JUN-2002;
            NEW ENGLAND BIOLABS INC
COMMENT     OS   Unknown
            PN   JP 2002517260-A/94
            PD   18-JUN-2002
            PF   11-JUN-1999 JP 2000553622
            PR   12-JUN-1998 US    60/089086,12-JUN-1998 US    60/089101 PI
            ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
            C12Q1/68,C12N15/09,C12N15/00
            CC   Description of Unknown Organism: Consensus sequence CC
            Position 1 - R = A or G; Position 2, 3 & 4 - Y = C or T FH   Key
                     Location/Qualifiers
            FT   source          1. .7
            FT                   /organism='Unknown'.
FEATURES                Location/Qualifiers
     source             1. .7
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          2 YYY 4


RESULT 98
BD211370/c
LOCUS       BD211370                  7 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Method of finding restriction enzyme.
ACCESSION   BD211370
VERSION     BD211370.1  GI:33021140
KEYWORDS    JP 2002517260-A/94.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 7)
  AUTHORS   Raleigh,E.A., Vaisvila,R. and Morgan,R.D.
  TITLE     Method of finding restriction enzyme
  JOURNAL   Patent: JP 2002517260-A 94 18-JUN-2002;
            NEW ENGLAND BIOLABS INC
COMMENT     OS   Unknown
            PN   JP 2002517260-A/94
            PD   18-JUN-2002
            PF   11-JUN-1999 JP 2000553622
            PR   12-JUN-1998 US    60/089086,12-JUN-1998 US    60/089101 PI
            ELISABETH A RALEIGH,ROMUALDAS VAISVILA,RICHARD D MORGAN PC
            C12Q1/68,C12N15/09,C12N15/00
            CC   Description of Unknown Organism: Consensus sequence CC
            Position 1 - R = A or G; Position 2, 3 & 4 - Y = C or T FH   Key
                     Location/Qualifiers
            FT   source          1. .7
            FT                   /organism='Unknown'.
FEATURES                Location/Qualifiers
     source             1. .7
                        /organism="unidentified"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          4 RRR 2


RESULT 99
E64766
LOCUS       E64766                    8 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Chemically synthesized artificial promoter for realizing high-level
             expression of introduced gene and method for synthesizing the
            same.
ACCESSION   E64766
VERSION     E64766.1  GI:18628529
KEYWORDS    JP 2000139477-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Tori,R., Sawanto,S.B., Synge,P.K. and Guputa,S.K.
  TITLE     Chemically synthesized artificial promoter for realizing high-level
            expression of introduced gene and method for synthesizing the same
  JOURNAL   Patent: JP 2000139477-A 7 23-MAY-2000;
            COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2000139477-A/7
            PD   23-MAY-2000
            PF   27-APR-1999 JP 1999119227
            PR   09-NOV-1998 IN      3322/98
            PI   RAKESH TORI,SALLY BISHUWANATO SAWANTO,PURAJUNNA KUMAR SYNGE,
            PI   SHIFU KUMAR GUPUTA
            PC   C12N15/09,C12N5/10,C12N15/00,C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .8
            FT                   /organism='Artificial Sequence'.
FEATURES                Location/Qualifiers
     source             1. .8
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          1 RRR 3
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RESULT 100
E64766/c
LOCUS       E64766                    8 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Chemically synthesized artificial promoter for realizing high-level
            expression of introduced gene and method for synthesizing the
            same.
ACCESSION   E64766
VERSION     E64766.1  GI:18628529
KEYWORDS    JP 2000139477-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Tori,R., Sawanto,S.B., Synge,P.K. and Guputa,S.K.
  TITLE     Chemically synthesized artificial promoter for realizing high-level
            expression of introduced gene and method for synthesizing the same
  JOURNAL   Patent: JP 2000139477-A 7 23-MAY-2000;
            COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2000139477-A/7
            PD   23-MAY-2000
            PF   27-APR-1999 JP 1999119227
            PR   09-NOV-1998 IN      3322/98
            PI   RAKESH TORI,SALLY BISHUWANATO SAWANTO,PURAJUNNA KUMAR SYNGE,
            PI   SHIFU KUMAR GUPUTA
            PC   C12N15/09,C12N5/10,C12N15/00,C12N5/00
            CC
            FH   Key             Location/Qualifiers
            FT   source          1. .8
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          8 YYY 6


RESULT 101
AX046162
LOCUS       AX046162                  8 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 41 from Patent WO0066734.
ACCESSION   AX046162
VERSION     AX046162.1  GI:11344245
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Lee,M.E. and Yet,S.F.
  TITLE     Methods of treating hypertension
  JOURNAL   Patent: WO 0066734-A 41 09-NOV-2000;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="consensus~consensus"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          6 YYY 8


RESULT 102
AX046162/c
LOCUS       AX046162                  8 bp    DNA     linear   PAT 24-NOV-2000
DEFINITION  Sequence 41 from Patent WO0066734.
ACCESSION   AX046162
VERSION     AX046162.1  GI:11344245
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Lee,M.E. and Yet,S.F.
  TITLE     Methods of treating hypertension
  JOURNAL   Patent: WO 0066734-A 41 09-NOV-2000;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US)
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
                     /note="consensus~consensus"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          8 RRR 6


RESULT 103
BD084758
LOCUS       BD084758                  8 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human nerve growth factor exon 1 and exon 3 promoters.
ACCESSION   BD084758
VERSION     BD084758.1  GI:22630368
KEYWORDS    JP 2001521375-A/56.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Linnik,M.D., Racke,M.M., Krakowsky,J.M. and Subramaniam,A.
  TITLE     Human nerve growth factor exon 1 and exon 3 promoters
  JOURNAL   Patent: JP 2001521375-A 56 06-NOV-2001;
            HOECHST MARION ROUSSEL INC
COMMENT     OS   Unidentified
            PN   JP 2001521375-A/56
            PD   06-NOV-2001
            PF   12-JAN-1998 JP 1998534446
            PR   06-FEB-1997 US    60/038212
            PI   MATTHEW D LINNIK,MARGARET M RACKE,JOAN M KRAKOWSKY,ARUN  PI
            SUBRAMANIAM
            PC   C07K14/48,C12Q1/68
            CC   Strandedness: Double;
            CC   Topology: Unknown;
            CC   Human nerve growth factor exon 1 and exon 3 promoters FH   Key
                       Location/Qualifiers
            FT   source          1. .8
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .8
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN
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  Query Match           30.0%;  Score 3;  DB 6;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          6 WWG 8


RESULT 104
BD084758/c
LOCUS       BD084758                  8 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human nerve growth factor exon 1 and exon 3 promoters.
ACCESSION   BD084758
VERSION     BD084758.1  GI:22630368
KEYWORDS    JP 2001521375-A/56.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 8)
  AUTHORS   Linnik,M.D., Racke,M.M., Krakowsky,J.M. and Subramaniam,A.
  TITLE     Human nerve growth factor exon 1 and exon 3 promoters
  JOURNAL   Patent: JP 2001521375-A 56 06-NOV-2001;
            HOECHST MARION ROUSSEL INC
COMMENT     OS   Unidentified
            PN   JP 2001521375-A/56
            PD   06-NOV-2001
            PF   12-JAN-1998 JP 1998534446
            PR   06-FEB-1997 US    60/038212
            PI   MATTHEW D LINNIK,MARGARET M RACKE,JOAN M KRAKOWSKY,ARUN  PI
            SUBRAMANIAM
            PC   C07K14/48,C12Q1/68
            CC   Strandedness: Double;
            CC   Topology: Unknown;
            CC   Human nerve growth factor exon 1 and exon 3 promoters FH   Key
                    Location/Qualifiers
            FT   source          1. .8
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .8
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          8 CWW 6


RESULT 105
A37861
LOCUS       A37861                    10 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 4 from Patent WO9408025.
ACCESSION   A37861
VERSION     A37861.1  GI:2294541
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Benech,P., Perez,C. and Wietzerbin,J.
  TITLE     DNA SEQUENCES INVOLVED IN THE TRANSCRIPTION OF GENES UNDER THE
            EFFECT OF INDUCERS, AND BIOLOGICAL APPLICATIONS THEREOF
  JOURNAL   Patent: WO 9408025-A 4 14-APR-1994;
            INST NAT SANTE RECH MED (FR)
COMMENT     Other publication FR 2696181 940401.
FEATURES            Location/Qualifiers
     source         1. .10
                    /organism="unidentified"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32644"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 106
A37861/c
LOCUS       A37861                    10 bp    DNA     linear   PAT 05-MAR-1997
DEFINITION  Sequence 4 from Patent WO9408025.
ACCESSION   A37861
VERSION     A37861.1  GI:2294541
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Benech,P., Perez,C. and Wietzerbin,J.
  TITLE     DNA SEQUENCES INVOLVED IN THE TRANSCRIPTION OF GENES UNDER THE
            EFFECT OF INDUCERS, AND BIOLOGICAL APPLICATIONS THEREOF
  JOURNAL   Patent: WO 9408025-A 4 14-APR-1994;
            INST NAT SANTE RECH MED (FR)
COMMENT     Other publication FR 2696181 940401.
FEATURES            Location/Qualifiers
     source         1. .10
                    /organism="unidentified"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32644"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          3 RRR 1


RESULT 107
AR074451
LOCUS       AR074451                  10 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 23 from patent US 5955075.
ACCESSION   AR074451
VERSION     AR074451.1  GI:10001206
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Method of inhibiting tumor growth using antibodies to MN protein
  JOURNAL   Patent: US 5955075-A 23 21-SEP-1999;
FEATURES            Location/Qualifiers
     source         1. .10
                    /organism="unknown"
                    /mol_type="unassigned DNA"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
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                ||| 
Db          1 YYY 3


RESULT 108
AR074451/c
LOCUS       AR074451                 10 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 23 from patent US 5955075.
ACCESSION   AR074451
VERSION     AR074451.1  GI:10001206
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Method of inhibiting tumor growth using antibodies to MN protein
  JOURNAL   Patent: US 5955075-A 23 21-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 109
AR081131
LOCUS       AR081131                 10 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 23 from patent US 5972353.
ACCESSION   AR081131
VERSION     AR081131.1  GI:10007859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN proteins, polypeptides, fusion proteins and fusion polypeptides
  JOURNAL   Patent: US 5972353-A 23 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 110
AR081131/c
LOCUS       AR081131                 10 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 23 from patent US 5972353.
ACCESSION   AR081131
VERSION     AR081131.1  GI:10007859
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN proteins, polypeptides, fusion proteins and fusion polypeptides
  JOURNAL   Patent: US 5972353-A 23 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 111
AR085328
LOCUS       AR085328                 10 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 23 from patent US 5981711.
ACCESSION   AR085328
VERSION     AR085328.1  GI:10012097
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN-specific antibodies and hybridomas
  JOURNAL   Patent: US 5981711-A 23 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 112
AR085328/c
LOCUS       AR085328                 10 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 23 from patent US 5981711.
ACCESSION   AR085328
VERSION     AR085328.1  GI:10012097
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN-specific antibodies and hybridomas
  JOURNAL   Patent: US 5981711-A 23 09-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
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Db          10 RRR 8


RESULT 113
AR088076
LOCUS       AR088076                  10 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 23 from patent US 5989838.
ACCESSION   AR088076
VERSION     AR088076.1  GI:10014839
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Immunological methods of detecting MN proteins and MN polypeptides
  JOURNAL   Patent: US 5989838-A 23 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 114
AR088076/c
LOCUS       AR088076                  10 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 23 from patent US 5989838.
ACCESSION   AR088076
VERSION     AR088076.1  GI:10014839
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Immunological methods of detecting MN proteins and MN polypeptides
  JOURNAL   Patent: US 5989838-A 23 23-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 115
AR104235
LOCUS       AR104235                  10 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 23 from patent US 6093548.
ACCESSION   AR104235
VERSION     AR104235.1  GI:12816943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Detection and quantitation of MN-specific antibodies
  JOURNAL   Patent: US 6093548-A 23 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 116
AR104235/c
LOCUS       AR104235                  10 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 23 from patent US 6093548.
ACCESSION   AR104235
VERSION     AR104235.1  GI:12816943
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     Detection and quantitation of MN-specific antibodies
  JOURNAL   Patent: US 6093548-A 23 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 117
AR110243
LOCUS       AR110243                  10 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 47 from patent US 6114311.
ACCESSION   AR110243
VERSION     AR110243.1  GI:12826519
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Method for modulating smooth muscle cell proliferation
  JOURNAL   Patent: US 6114311-A 47 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4
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RESULT 118
AR110243/c
LOCUS       AR110243                  10 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 47 from patent US 6114311.
ACCESSION   AR110243
VERSION     AR110243.1  GI:12826519
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Method for modulating smooth muscle cell proliferation
  JOURNAL   Patent: US 6114311-A 47 05-SEP-2000;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          4 WWG 2


RESULT 119
AR134895
LOCUS       AR134895                  10 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 11 from patent US 6194211.
ACCESSION   AR134895
VERSION     AR134895.1  GI:14123800
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Richards,C.Ann. and Huber,B.
  TITLE     Transcriptional regulatory sequence of carcinoembryonic antigen for
            expression targeting
  JOURNAL   Patent: US 6194211-A 11 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 120
AR134895/c
LOCUS       AR134895                  10 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 11 from patent US 6194211.
ACCESSION   AR134895
VERSION     AR134895.1  GI:14123800
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Richards,C.Ann. and Huber,B.
  TITLE     Transcriptional regulatory sequence of carcinoembryonic antigen for
            expression targeting
  JOURNAL   Patent: US 6194211-A 11 27-FEB-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7


RESULT 121
AR139421
LOCUS       AR139421                  10 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6207377.
ACCESSION   AR139421
VERSION     AR139421.1  GI:14481917
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Wayne,J. and Xu,S.-y.
  TITLE     Method for construction of thermus-E. coli shuttle vectors and
            identification of two Thermus plasmid replication origins
  JOURNAL   Patent: US 6207377-A 1 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          1 RRC 3


RESULT 122
AR139421/c
LOCUS       AR139421                  10 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 1 from patent US 6207377.
ACCESSION   AR139421
VERSION     AR139421.1  GI:14481917
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Wayne,J. and Xu,S.-y.
  TITLE     Method for construction of thermus-E. coli shuttle vectors and
            identification of two Thermus plasmid replication origins
  JOURNAL   Patent: US 6207377-A 1 27-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 123
AR143499
LOCUS       AR143499                  10 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 23 from patent US 6204370.
ACCESSION   AR143499
VERSION     AR143499.1  GI:15104785
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6204370-A 23 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 124
AR143499/c
LOCUS       AR143499                  10 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 23 from patent US 6204370.
ACCESSION   AR143499
VERSION     AR143499.1  GI:15104785
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6204370-A 23 20-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 125
AR170002
LOCUS       AR170002                  10 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 47 from patent US 6291211.
ACCESSION   AR170002
VERSION     AR170002.1  GI:17907961
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Promoter for smooth muscle cell expression
  JOURNAL   Patent: US 6291211-A 47 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 126
AR170002/c
LOCUS       AR170002                  10 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 47 from patent US 6291211.
ACCESSION   AR170002
VERSION     AR170002.1  GI:17907961
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Promoter for smooth muscle cell expression
  JOURNAL   Patent: US 6291211-A 47 18-SEP-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          4 WWG 2


RESULT 127
AR171403
LOCUS       AR171403                  10 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 23 from patent US 6297041.
ACCESSION   AR171403
VERSION     AR171403.1  GI:17910353
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297041-A 23 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
```

```
              |||
Db          1 YYY 3


RESULT 128
AR171403/c
LOCUS       AR171403                  10 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 23 from patent US 6297041.
ACCESSION   AR171403
VERSION     AR171403.1  GI:17910353
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297041-A 23 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 129
AR171574
LOCUS       AR171574                  10 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 23 from patent US 6297051.
ACCESSION   AR171574
VERSION     AR171574.1  GI:17910524
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297051-A 23 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 130
AR171574/c
LOCUS       AR171574                  10 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 23 from patent US 6297051.
ACCESSION   AR171574
VERSION     AR171574.1  GI:17910524
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: US 6297051-A 23 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 131
AR171811
LOCUS       AR171811                  10 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 47 from patent US 6297221.
ACCESSION   AR171811
VERSION     AR171811.1  GI:17910761
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Method for promoting angiogenesis with a nucleic acid construct
            comprising an SM22.alpha.0 promoter
  JOURNAL   Patent: US 6297221-A 47 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 132
AR171811/c
LOCUS       AR171811                  10 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 47 from patent US 6297221.
ACCESSION   AR171811
VERSION     AR171811.1  GI:17910761
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Method for promoting angiogenesis with a nucleic acid construct
            comprising an SM22.alpha.0 promoter
  JOURNAL   Patent: US 6297221-A 47 02-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          5 WWG 7
              |||
Db          4 WWG 2


RESULT 133
BD189505
LOCUS       BD189505                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION.
ACCESSION   BD189505
VERSION     BD189505.1  GI:32999244
KEYWORDS    JP 2003009894-A/38.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
  JOURNAL   Patent: JP 2003009894-A 38 14-JAN-2003;
            ARCH DEVELOPMENT CORPORATION
COMMENT     OS   Artificial Sequence
            PN   JP 2003009894-A/38
            PD   14-JAN-2003
            PF   10-MAY-2002 JP 2002136310
            PR   07-OCT-1996 US    08/726807
            PI   michael s parmacek,julian solway
            CC   Description of Artificial Sequence: PRIMER
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .10
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 134
BD189505/c
LOCUS       BD189505                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION.
ACCESSION   BD189505
VERSION     BD189505.1  GI:32999244
KEYWORDS    JP 2003009894-A/38.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
  JOURNAL   Patent: JP 2003009894-A 38 14-JAN-2003;
            ARCH DEVELOPMENT CORPORATION
COMMENT     OS   Artificial Sequence
            PN   JP 2003009894-A/38
            PD   14-JAN-2003
            PF   10-MAY-2002 JP 2002136310
            PR   07-OCT-1996 US    08/726807
            PI   michael s parmacek,julian solway
            CC   Description of Artificial Sequence: PRIMER
            FH   Key             Location/Qualifiers.
FEATURES                Location/Qualifiers
     source             1. .10
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          4 WWG 2


RESULT 135
BD243164
LOCUS       BD243164                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  MN gene and protein.
ACCESSION   BD243164
VERSION     BD243164.1  GI:33052934
KEYWORDS    JP 2002528085-A/13.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: JP 2002528085-A 13 03-SEP-2002;
            INSTITUTE OF VIROLOGY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002528085-A/13
            PD   03-SEP-2002
            PF   22-OCT-1999 JP 2000578465
            PR   23-OCT-1998 US    09/177776,23-OCT-1998 US    09/178115 PI
            JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
            C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P35/00, PC
            C07K14/47,
            PC   C12Q1/02,G01N33/566//(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
            CC   MN gene and protein
            FH   Key             Location/Qualifiers
            FT   misc_feature    (1). .(10).
FEATURES                Location/Qualifiers
     source             1. .10
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 136
BD243164/c
LOCUS       BD243164                  10 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  MN gene and protein.
ACCESSION   BD243164
VERSION     BD243164.1  GI:33052934
KEYWORDS    JP 2002528085-A/13.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
  TITLE     MN gene and protein
  JOURNAL   Patent: JP 2002528085-A 13 03-SEP-2002;
            INSTITUTE OF VIROLOGY
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002528085-A/13
            PD   03-SEP-2002
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            PF   22-OCT-1999 JP 2000578465
            PR   23-OCT-1998 US    09/177776,23-OCT-1998 US    09/178115 PI
            JAN ZAVADA,SILVIA PASTOREKOVA,JAROMIR PASTOREK PC
            C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P35/00, PC
            C07K14/47,
            PC   C12Q1/02,G01N33/566//(C12Q1/02,C12R1:91),C12N15/00,A61K37/02
            CC   MN gene and protein
            FH   Key             Location/Qualifiers
            FT   misc_feature    (1). .(10).
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 137
CQ814915
LOCUS       CQ814915                  10 bp    DNA     linear   PAT 24-MAY-2004
DEFINITION  Sequence 1 from Patent WO2004039980.
ACCESSION   CQ814915
VERSION     CQ814915.1  GI:47604076
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Treisman,R.H., Miralles-Arenas,F., Zaromytidou,A.I. and Posern,G.
  TITLE     Agents modulating mal activity
  JOURNAL   Patent: WO 2004039980-A 1 13-MAY-2004;
            Cancer Research Technology Limited (GB)
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Consensus sequence of the CArG box"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 138
CQ814915/c
LOCUS       CQ814915                  10 bp    DNA     linear   PAT 24-MAY-2004
DEFINITION  Sequence 1 from Patent WO2004039980.
ACCESSION   CQ814915
VERSION     CQ814915.1  GI:47604076
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Treisman,R.H., Miralles-Arenas,F., Zaromytidou,A.I. and Posern,G.
  TITLE     Agents modulating mal activity
  JOURNAL   Patent: WO 2004039980-A 1 13-MAY-2004;
            Cancer Research Technology Limited (GB)
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Consensus sequence of the CArG box"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7


RESULT 139
I72403
LOCUS       I72403                    10 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 34 from patent US 5683985.
ACCESSION   I72403
VERSION     I72403.1  GI:3008542
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chu,B.Chen.Fei. and Orgel,L.
  TITLE     Oligonucleotide decoys and methods relating thereto
  JOURNAL   Patent: US 5683985-A 34 04-NOV-1997;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 140
I72403/c
LOCUS       I72403                    10 bp    DNA     linear   PAT 03-APR-1998
DEFINITION  Sequence 34 from patent US 5683985.
ACCESSION   I72403
VERSION     I72403.1  GI:3008542
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Chu,B.Chen.Fei. and Orgel,L.
  TITLE     Oligonucleotide decoys and methods relating thereto
  JOURNAL   Patent: US 5683985-A 34 04-NOV-1997;
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7
```

```
RESULT 141
I84595
LOCUS       I84595                  10 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 1 from patent US 5695977.
ACCESSION   I84595
VERSION     I84595.1  GI:3022115
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 1 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          7 YYY 9


RESULT 142
I84595/c
LOCUS       I84595                  10 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 1 from patent US 5695977.
ACCESSION   I84595
VERSION     I84595.1  GI:3022115
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 1 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          9 RRR 7


RESULT 143
I84606
LOCUS       I84606                  10 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 12 from patent US 5695977.
ACCESSION   I84606
VERSION     I84606.1  GI:3022126
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 12 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          7 RRR 9


RESULT 144
I84606/c
LOCUS       I84606                  10 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 12 from patent US 5695977.
ACCESSION   I84606
VERSION     I84606.1  GI:3022126
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 12 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          9 YYY 7


RESULT 145
AR220243
LOCUS       AR220243                10 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from patent US 6423693.
ACCESSION   AR220243
VERSION     AR220243.1  GI:23324971
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Schwartz,R.J., Draghia-Akli,R., Li,X. and Eastman,E.M.
  TITLE     Growth hormone releasing hormone expression system and methods of
            use, including use in animals
  JOURNAL   Patent: US 6423693-A 3 23-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4
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RESULT 146
AR220243/c
LOCUS       AR220243                  10 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 3 from patent US 6423693.
ACCESSION   AR220243
VERSION     AR220243.1  GI:23324971
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Schwartz,R.J., Draghia-Akli,R., Li,X. and Eastman,E.M.
  TITLE     Growth hormone releasing hormone expression system and methods of
            use, including use in animals
  JOURNAL   Patent: US 6423693-A 3 23-JUL-2002;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7


RESULT 147
AR264148
LOCUS       AR264148                  10 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 47 from patent US 6331527.
ACCESSION   AR264148
VERSION     AR264148.1  GI:28076219
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Promoter smooth muscle cell expression
  JOURNAL   Patent: US 6331527-A 47 18-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 148
AR264148/c
LOCUS       AR264148                  10 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 47 from patent US 6331527.
ACCESSION   AR264148
VERSION     AR264148.1  GI:28076219
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Promoter smooth muscle cell expression
  JOURNAL   Patent: US 6331527-A 47 18-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          4 WWG 2


RESULT 149
AR362282
LOCUS       AR362282                  10 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 1 from patent US 5164316.
ACCESSION   AR362282
VERSION     AR362282.1  GI:34422165
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   McPherson,J.C. and Kay,R.
  TITLE     DNA construct for enhancing the efficiency of transcription
  JOURNAL   Patent: US 5164316-A 1 17-NOV-1992;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          8 WWG 10


RESULT 150
AR362282/c
LOCUS       AR362282                  10 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 1 from patent US 5164316.
ACCESSION   AR362282
VERSION     AR362282.1  GI:34422165
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   McPherson,J.C. and Kay,R.
  TITLE     DNA construct for enhancing the efficiency of transcription
  JOURNAL   Patent: US 5164316-A 1 17-NOV-1992;
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db         10 CWW 8
```

```
RESULT 151
AX412946
LOCUS       AX412946                 10 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 710 from Patent WO0222675.
ACCESSION   AX412946
VERSION     AX412946.1  GI:21445404
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Glazebrook,J., Wang,X., Dangl,J.L., Eulgem,T. and Zhu,T.
  TITLE     Plant genes, the expression of which are altered by pathogen
            infection
  JOURNAL   Patent: WO 0222675-A 710 21-MAR-2002;
            Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT
            CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,
            Jeffrey L. (US) ; Eulgem, Thomas (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3702"
     misc_feature    5. .6
                     /note="w = adenine or thymine"
     misc_feature    9
                     /note="w = adenine or thymine"
     misc_feature    10
                     /note="y = cytosine or thymine"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          4 CWW 6


RESULT 152
AX412946/c
LOCUS       AX412946                 10 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 710 from Patent WO0222675.
ACCESSION   AX412946
VERSION     AX412946.1  GI:21445404
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Glazebrook,J., Wang,X., Dangl,J.L., Eulgem,T. and Zhu,T.
  TITLE     Plant genes, the expression of which are altered by pathogen
            infection
  JOURNAL   Patent: WO 0222675-A 710 21-MAR-2002;
            Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT
            CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,
            Jeffrey L. (US) ; Eulgem, Thomas (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="Arabidopsis thaliana"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:3702"
     misc_feature    5. .6
                     /note="w = adenine or thymine"
     misc_feature    9
                     /note="w = adenine or thymine"
     misc_feature    10
                     /note="y = cytosine or thymine"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          6 WWG 4


RESULT 153
AX497559
LOCUS       AX497559                 10 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 103 from Patent WO0233126.
ACCESSION   AX497559
VERSION     AX497559.1  GI:23342829
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Grenier,J.K., Marshall,D.J., Prudent,J.R., Richmond,C.S.,
            Roesch,E.B., Scherrer,C.W., Sherrill,C.B. and Ptacin,J.L.
  TITLE     Solid support assay systems and methods utilizing non-standard
            bases
  JOURNAL   Patent: WO 0233126-A 103 25-APR-2002;
            Eragen Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotides"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYY 9
              |||
Db          1 GYY 3


RESULT 154
AX497559/c
LOCUS       AX497559                 10 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 103 from Patent WO0233126.
ACCESSION   AX497559
VERSION     AX497559.1  GI:23342829
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Grenier,J.K., Marshall,D.J., Prudent,J.R., Richmond,C.S.,
            Roesch,E.B., Scherrer,C.W., Sherrill,C.B. and Ptacin,J.L.
  TITLE     Solid support assay systems and methods utilizing non-standard
            bases
  JOURNAL   Patent: WO 0233126-A 103 25-APR-2002;
            Eragen Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .10
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic Oligonucleotides"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
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  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          3 RRC 1


RESULT 155
BD009036
LOCUS       BD009036                  10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Promoter for smooth muscle cell expression.
ACCESSION   BD009036
VERSION     BD009036.1  GI:18637409
KEYWORDS    JP 2001502899-A/38.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Promoter for smooth muscle cell expression
  JOURNAL   Patent: JP 2001502899-A 38 06-MAR-2001;
            ARCH DEVELOPMENT CORP
COMMENT     OS   Unidentified
            PN   JP 2001502899-A/38
            PD   06-MAR-2001
            PF   29-AUG-1997 JP 1998517528
            PR   07-OCT-1996 US    08/726807
            PI   MICHAEL S PARMACEK,JULIAN SOLWAY
            PC   C07K14/47
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   modified base   3. .8.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 156
BD009036/c
LOCUS       BD009036                  10 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Promoter for smooth muscle cell expression.
ACCESSION   BD009036
VERSION     BD009036.1  GI:18637409
KEYWORDS    JP 2001502899-A/38.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Parmacek,M.S. and Solway,J.
  TITLE     Promoter for smooth muscle cell expression
  JOURNAL   Patent: JP 2001502899-A 38 06-MAR-2001;
            ARCH DEVELOPMENT CORP
COMMENT     OS   Unidentified
            PN   JP 2001502899-A/38
            PD   06-MAR-2001
            PF   29-AUG-1997 JP 1998517528
            PR   07-OCT-1996 US    08/726807
            PI   MICHAEL S PARMACEK,JULIAN SOLWAY
            PC   C07K14/47
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   modified base   3. .8.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          4 WWG 2


RESULT 157
BD063695
LOCUS       BD063695                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Glutathione-S-conjugate transport in plants.
ACCESSION   BD063695
VERSION     BD063695.1  GI:22609298
KEYWORDS    JP 2001504700-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Rea,P.A., Lu,Y.P. and Li,Z.S.
  TITLE     Glutathione-S-conjugate transport in plants
  JOURNAL   Patent: JP 2001504700-A 7 10-APR-2001;
            THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
COMMENT     PN   JP 2001504700-A/7
            PD   10-APR-2001
            PF   18-NOV-1997 JP 1998523910
            PR   18-NOV-1996 US    60/031040,08-OCT-1997 US    60/061328 PI
            PHILIP A REA,YU PING LU,ZE SHENG LI
            PC   A01H5/00,C07K14/415,C07K16/16,C12N1/13,C12N1/21,C12N5/10, PC
            C12N15/29,
            PC   C12N15/64,C12N15/82
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          7 WWG 9


RESULT 158
BD063695/c
LOCUS       BD063695                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Glutathione-S-conjugate transport in plants.
ACCESSION   BD063695
VERSION     BD063695.1  GI:22609298
KEYWORDS    JP 2001504700-A/7.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Rea,P.A., Lu,Y.P. and Li,Z.S.
  TITLE     Glutathione-S-conjugate transport in plants
```

```
  JOURNAL   Patent: JP 2001504700-A 7 10-APR-2001;
            THE TRUSTEES OF THE UNIVERSITY OF PENNSYLVANIA
COMMENT     PN   JP 2001504700-A/7
            PD   10-APR-2001
            PF   18-NOV-1997 JP 1998523910
            PR   18-NOV-1996 US    60/031040,08-OCT-1997 US    60/061328 PI
            PHILIP A REA,YU PING LU,ZE SHENG LI
            PC   A01H5/00,C07K14/415,C07K16/16,C12N1/13,C12N1/21,C12N5/10, PC
            C12N15/29,
            PC   C12N15/64,C12N15/82
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7


RESULT 159
BD073429
LOCUS       BD073429                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Expression system of GHRH and utilization method.
ACCESSION   BD073429
VERSION     BD073429.1  GI:22619032
KEYWORDS    JP 2001511353-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Schwartz,R.J., Akli,R.D., Li,X. and Eastman,E.M.
  TITLE     Expression system of GHRH and utilization method
  JOURNAL   Patent: JP 2001511353-A 3 14-AUG-2001;
            BARENTIS INC
COMMENT     OS   pSK-GHRH
            PN   JP 2001511353-A/3
            PD   14-AUG-2001
            PF   24-JUL-1998 JP 2000504270
            PR   24-JUL-1997 US    60/053609,20-OCT-1997 US    60/062608 PI
            ROBERT J SCHWARTZ,RUXANDRA DRAGHIA AKLI,XUYANG LI,ERIC M  PI
            EASTMAN
            PC   C12N15/09,A01K67/027,C12N5/10//A61K38/22,C07K14/60,C12N15/00,
            PC   C12N5/00,
            PC   A61K37/24
            CC   The letter 'w' stands for a or t.
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='pSK-GHRH'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 160
BD073429/c
LOCUS       BD073429                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Expression system of GHRH and utilization method.
ACCESSION   BD073429
VERSION     BD073429.1  GI:22619032
KEYWORDS    JP 2001511353-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Schwartz,R.J., Akli,R.D., Li,X. and Eastman,E.M.
  TITLE     Expression system of GHRH and utilization method
  JOURNAL   Patent: JP 2001511353-A 3 14-AUG-2001;
            BARENTIS INC
COMMENT     OS   pSK-GHRH
            PN   JP 2001511353-A/3
            PD   14-AUG-2001
            PF   24-JUL-1998 JP 2000504270
            PR   24-JUL-1997 US    60/053609,20-OCT-1997 US    60/062608 PI
            ROBERT J SCHWARTZ,RUXANDRA DRAGHIA AKLI,XUYANG LI,ERIC M  PI
            EASTMAN
            PC   C12N15/09,A01K67/027,C12N5/10//A61K38/22,C07K14/60,C12N15/00,
            PC   C12N5/00,
            PC   A61K37/24
            CC   The letter 'w' stands for a or t.
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='pSK-GHRH'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7


RESULT 161
BD091328
LOCUS       BD091328                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  In vitro differentiation of vascular smooth muscle cells, and
            method and reagent related thereto.
ACCESSION   BD091328
VERSION     BD091328.1  GI:22636938
KEYWORDS    JP 2001520877-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Lee,A.M.E., Jain,M. and Watanabe,M.
  TITLE     In vitro differentiation of vascular smooth muscle cells, and
            method and reagent related thereto
  JOURNAL   Patent: JP 2001520877-A 3 06-NOV-2001;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE
COMMENT     OS   Artificial Sequence
            PN   JP 2001520877-A/3
            PD   06-NOV-2001
            PF   28-OCT-1998 JP 2000518057
            PR   28-OCT-1997 US    60/063363,02-APR-1998 US    60/080420 PR
            14-AUG-1998 US    60/096685
            PI   ARTHUR M E LEE,MUKESH JAIN,MASAFUMI WATANABE
            PC   C12N15/09,C12N5/06,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: CArG box
            FH   Key             Location/Qualifiers
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            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 162
BD091328/c
LOCUS       BD091328                  10 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  In vitro differentiation of vascular smooth muscle cells, and
            method and reagent related thereto.
ACCESSION   BD091328
VERSION     BD091328.1  GI:22636938
KEYWORDS    JP 2001520877-A/3.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 10)
  AUTHORS   Lee,A.M.E., Jain,M. and Watanabe,M.
  TITLE     In vitro differentiation of vascular smooth muscle cells, and
            method and reagent related thereto
  JOURNAL   Patent: JP 2001520877-A 3 06-NOV-2001;
            PRESIDENT AND FELLOWS OF HARVARD COLLEGE
COMMENT     OS   Artificial Sequence
            PN   JP 2001520877-A/3
            PD   06-NOV-2001
            PF   28-OCT-1998 JP 2000518057
            PR   28-OCT-1997 US    60/063363,02-APR-1998 US    60/080420 PR
            14-AUG-1998 US    60/096685
            PI   ARTHUR M E LEE,MUKESH JAIN,MASAFUMI WATANABE
            PC   C12N15/09,C12N5/06,C12N15/00,C12N5/00
            CC   Description of Artificial Sequence: CArG box
            FH   Key             Location/Qualifiers
            FT   source          1. .10
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .10
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7


RESULT 163
I84607
LOCUS       I84607                    11 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 13 from patent US 5695977.
ACCESSION   I84607
VERSION     I84607.1  GI:3022127
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 13 09-DEC-1997;
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          8 RRR 10


RESULT 164
I84607/c
LOCUS       I84607                    11 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 13 from patent US 5695977.
ACCESSION   I84607
VERSION     I84607.1  GI:3022127
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 13 09-DEC-1997;
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         10 YYY 8


RESULT 165
AX012240
LOCUS       AX012240                  11 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 2 from Patent WO9955856.
ACCESSION   AX012240
VERSION     AX012240.1  GI:9998301
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE     Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 9955856-A 2 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES              Location/Qualifiers
     source           1. .11
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="synthetic nucleic acid"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 11;
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          1 RRR 3


RESULT 166
AX012240/c
LOCUS       AX012240                  11 bp    DNA     linear   PAT 06-SEP-2000
DEFINITION  Sequence 2 from Patent WO9955856.
ACCESSION   AX012240
VERSION     AX012240.1  GI:9998301
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Ananvoranich,S., Lafontaine,D. and Perreault,J.P.
  TITLE     Nucleic acid enzyme for rna cleavage
  JOURNAL   Patent: WO 9955856-A 2 04-NOV-1999;
            ANANVORANICH SIRINART (CA); LAFONTAINE DANIEL (CA); PERREAULT JEAN
            PIERRE (CA); UNIV SHERBROOKE (CA)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="synthetic nucleic acid"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          3 YYY 1


RESULT 167
AX711145
LOCUS       AX711145                  11 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 445 from Patent EP1288296.
ACCESSION   AX711145
VERSION     AX711145.1  GI:29787526
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 445 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          3 WWG 5


RESULT 168
AX711145/c
LOCUS       AX711145                  11 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 445 from Patent EP1288296.
ACCESSION   AX711145
VERSION     AX711145.1  GI:29787526
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 445 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          5 CWW 3


RESULT 169
AX711146
LOCUS       AX711146                  11 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 446 from Patent EP1288296.
ACCESSION   AX711146
VERSION     AX711146.1  GI:29787527
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 446 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match            30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          7 CWW 9


RESULT 170
AX711146/c
LOCUS       AX711146                  11 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 446 from Patent EP1288296.
ACCESSION   AX711146
VERSION     AX711146.1  GI:29787527
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KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 446 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          9 WWG 7


RESULT 171
AX711147
LOCUS       AX711147                  11 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 447 from Patent EP1288296.
ACCESSION   AX711147
VERSION     AX711147.1  GI:29787528
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 447 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          7 CWW 9


RESULT 172
AX711147/c
LOCUS       AX711147                  11 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 447 from Patent EP1288296.
ACCESSION   AX711147
VERSION     AX711147.1  GI:29787528
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 447 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          5 CWW 3


RESULT 173
AX711148
LOCUS       AX711148                  11 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 448 from Patent EP1288296.
ACCESSION   AX711148
VERSION     AX711148.1  GI:29787529
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 448 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          3 WWG 5


RESULT 174
AX711148/c
LOCUS       AX711148                  11 bp    RNA     linear   PAT 11-APR-2003
DEFINITION  Sequence 448 from Patent EP1288296.
ACCESSION   AX711148
VERSION     AX711148.1  GI:29787529
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudycz,L.W.,
            Macejak,D.G. and Mamone,J.A.
  TITLE     Method and reagent for inhibiting HBV viral replication
  JOURNAL   Patent: EP 1288296-A 448 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
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                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          5 CWW 3


RESULT 175
I84596
LOCUS       I84596                    12 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 2 from patent US 5695977.
ACCESSION   I84596
VERSION     I84596.1  GI:3022116
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 2 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          9 YYY 11


RESULT 176
I84596/c
LOCUS       I84596                    12 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 2 from patent US 5695977.
ACCESSION   I84596
VERSION     I84596.1  GI:3022116
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 2 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         11 RRR 9


RESULT 177
I84608
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LOCUS       I84608                    12 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 14 from patent US 5695977.
ACCESSION   I84608
VERSION     I84608.1  GI:3022128
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 14 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          9 RRR 11


RESULT 178
I84608/c
LOCUS       I84608                    12 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 14 from patent US 5695977.
ACCESSION   I84608
VERSION     I84608.1  GI:3022128
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 14 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         11 YYY 9


RESULT 179
AX412933
LOCUS       AX412933                  12 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 697 from Patent WO0222675.
ACCESSION   AX412933
VERSION     AX412933.1  GI:21445391
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Glazebrook,J., Wang,X., Dangl,J.L., Eulgem,T. and Zhu,T.
  TITLE     Plant genes, the expression of which are altered by pathogen
            infection
  JOURNAL   Patent: WO 0222675-A 697 21-MAR-2002;
```

```
            Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT
            CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,
            Jeffrey L. (US) ; Eulgem, Thomas (US)
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="Arabidopsis thaliana"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:3702"
     misc_feature     7. .8
                      /note="w = adenine or thymine"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          6 CWW 8


RESULT 180
AX412933/c
LOCUS       AX412933                12 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 697 from Patent WO0222675.
ACCESSION   AX412933
VERSION     AX412933.1  GI:21445391
KEYWORDS    .
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Glazebrook,J., Wang,X., Dangl,J.L., Eulgem,T. and Zhu,T.
  TITLE     Plant genes, the expression of which are altered by pathogen
            infection
  JOURNAL   Patent: WO 0222675-A 697 21-MAR-2002;
            Syngenta Participations AG (CH) ; UNIVERSITY OF NORTH CAROLINA AT
            CHAPEL HILL (US) ; Glazebrook, Jan (US) ; Wang, Xun (US) ; Dangl,
            Jeffrey L. (US) ; Eulgem, Thomas (US)
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="Arabidopsis thaliana"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:3702"
     misc_feature     7. .8
                      /note="w = adenine or thymine"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          8 WWG 6


RESULT 181
AX816374
LOCUS       AX816374                12 bp    DNA     linear   PAT 09-DEC-2003
DEFINITION  Sequence 3 from Patent WO03066867.
ACCESSION   AX816374
VERSION     AX816374.1  GI:39646850
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Andreas,S. and Faust,N.
  TITLE     Genetically engineered phic31&minus;integrase genes
  JOURNAL   Patent: WO 03066867-A 3 14-AUG-2003;
            ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Description of Artificial Sequence: splice acceptor
                      sequence"
     misc_feature     1. .7
                      /note="Y is T or C"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 182
AX816374/c
LOCUS       AX816374                12 bp    DNA     linear   PAT 09-DEC-2003
DEFINITION  Sequence 3 from Patent WO03066867.
ACCESSION   AX816374
VERSION     AX816374.1  GI:39646850
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Andreas,S. and Faust,N.
  TITLE     Genetically engineered phic31&minus;integrase genes
  JOURNAL   Patent: WO 03066867-A 3 14-AUG-2003;
            ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES              Location/Qualifiers
     source           1. .12
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="Description of Artificial Sequence: splice acceptor
                      sequence"
     misc_feature     1. .7
                      /note="Y is T or C"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          7 RRR 5


RESULT 183
AX816375
LOCUS       AX816375                12 bp    DNA     linear   PAT 09-DEC-2003
DEFINITION  Sequence 4 from Patent WO03066867.
ACCESSION   AX816375
VERSION     AX816375.1  GI:39646851
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Andreas,S. and Faust,N.
  TITLE     Genetically engineered phic31&minus;integrase genes
  JOURNAL   Patent: WO 03066867-A 4 14-AUG-2003;
            ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES              Location/Qualifiers
     source           1. .12
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                     /organism="synthetic construct"
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                     site"
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                     /note="Y is T or C"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 184
AX816375/c
LOCUS       AX816375                  12 bp    DNA     linear   PAT 09-DEC-2003
DEFINITION  Sequence 4 from Patent WO03066867.
ACCESSION   AX816375
VERSION     AX816375.1  GI:39646851
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Andreas,S. and Faust,N.
  TITLE     Genetically engineered phic31&minus;integrase genes
  JOURNAL   Patent: WO 03066867-A 4 14-AUG-2003;
            ARTEMIS Pharmaceuticals GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Description of Artificial Sequence: splice acceptor
                     site"
     misc_feature    1. .7
                     /note="Y is T or C"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          7 RRR 5


RESULT 185
BD074027
LOCUS       BD074027                  12 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human glial cell-line derived neurotrophic factor promoter, vector
            containing the promoter, and method for screening a compound by the
            promoter.
ACCESSION   BD074027
VERSION     BD074027.1  GI:22619630
KEYWORDS    JP 2001512679-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Albert,B.P., Mels,J.R., Lee,W.O. and Nei,B.A.
  TITLE     Human glial cell-line derived neurotrophic factor promoter, vector
            containing the promoter, and method for screening a compound by the
            promoter
  JOURNAL   Patent: JP 2001512679-A 9 28-AUG-2001;
            F HOFFMANN LA ROCHE AG
COMMENT     OS   Unidentified
            PN   JP 2001512679-A/9
            PD   28-AUG-2001
            PF   23-JUL-1998 JP 2000506328
            PR   05-AUG-1997 US    60/054812,14-APR-1998 US    60/081751 PI
            BECKER PRESTON ALBERT,JOHNSON RADOLF MELS,WALTER OM LEE,BERITY
            PI   ADRIAN NEIL
            PC   C12N15/09,A61K45/00,A61P25/28,C12N5/10,C12Q1/68,G01N33/15, PC
             G01N33/50,
            PC   C12N15/00,C12N5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Human glial cell-line derived neurotrophic factor promoter,
            CC           vector
            CC   containing the promoter, and method for screening a compound
            CC           by the
            CC   promoter
            FH   Key             Location/Qualifiers
            FT   source          1. .12
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .12
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ORIGIN

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Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 186
BD074027/c
LOCUS       BD074027                  12 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Human glial cell-line derived neurotrophic factor promoter, vector
            containing the promoter, and method for screening a compound by the
            promoter.
ACCESSION   BD074027
VERSION     BD074027.1  GI:22619630
KEYWORDS    JP 2001512679-A/9.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Albert,B.P., Mels,J.R., Lee,W.O. and Nei,B.A.
  TITLE     Human glial cell-line derived neurotrophic factor promoter, vector
            containing the promoter, and method for screening a compound by the
            promoter
  JOURNAL   Patent: JP 2001512679-A 9 28-AUG-2001;
            F HOFFMANN LA ROCHE AG
COMMENT     OS   Unidentified
            PN   JP 2001512679-A/9
            PD   28-AUG-2001
            PF   23-JUL-1998 JP 2000506328
            PR   05-AUG-1997 US    60/054812,14-APR-1998 US    60/081751 PI
            BECKER PRESTON ALBERT,JOHNSON RADOLF MELS,WALTER OM LEE,BERITY
            PI   ADRIAN NEIL
            PC   C12N15/09,A61K45/00,A61P25/28,C12N5/10,C12Q1/68,G01N33/15, PC
             G01N33/50,
            PC   C12N15/00,C12N5/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Human glial cell-line derived neurotrophic factor promoter,
            CC           vector
            CC   containing the promoter, and method for screening a compound
            CC           by the
            CC   promoter
            FH   Key             Location/Qualifiers
            FT   source          1. .12
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 RRR 3
              |||
Db          7 RRR 5


RESULT 187
I27012
LOCUS       I27012                    13 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 33 from patent US 5563036.
ACCESSION   I27012
VERSION     I27012.1  GI:1817788
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Peterson,M.G., Baichwal,V.R. and Strulovici,B.
  TITLE     Transcription factor-DNA binding assay
  JOURNAL   Patent: US 5563036-A 33 08-OCT-1996;
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy          8 YYY 10
              |||
Db         11 YYY 13


RESULT 188
I27012/c
LOCUS       I27012                    13 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 33 from patent US 5563036.
ACCESSION   I27012
VERSION     I27012.1  GI:1817788
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Peterson,M.G., Baichwal,V.R. and Strulovici,B.
  TITLE     Transcription factor-DNA binding assay
  JOURNAL   Patent: US 5563036-A 33 08-OCT-1996;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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Qy          1 RRR 3
              |||
Db         13 RRR 11


RESULT 189
I84597
LOCUS       I84597                    13 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 3 from patent US 5695977.
ACCESSION   I84597
VERSION     I84597.1  GI:3022117
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 3 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .13
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         10 YYY 12


RESULT 190
I84597/c
LOCUS       I84597                    13 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 3 from patent US 5695977.
ACCESSION   I84597
VERSION     I84597.1  GI:3022117
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 3 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="unknown"
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ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 13;
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  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         12 RRR 10


RESULT 191
I84609
LOCUS       I84609                    13 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 15 from patent US 5695977.
ACCESSION   I84609
VERSION     I84609.1  GI:3022129
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
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  JOURNAL   Patent: US 5695977-A 15 09-DEC-1997;
FEATURES             Location/Qualifiers
     source          1. .13
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ORIGIN

  Query Match           30.0%;  Score 3;  DB 6;  Length 13;
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Qy          1 RRR 3
              |||
Db         10 RRR 12


RESULT 192
I84609/c
LOCUS       I84609                    13 bp    DNA     linear   PAT 04-APR-1998
DEFINITION  Sequence 15 from patent US 5695977.
ACCESSION   I84609
VERSION     I84609.1  GI:3022129
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Jurka,J.W.
  TITLE     Site directed recombination
  JOURNAL   Patent: US 5695977-A 15 09-DEC-1997;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          8 YYY 10
              |||
Db         12 YYY 10


RESULT 193
AX235305
LOCUS       AX235305                  13 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 7 from Patent WO0162967.
ACCESSION   AX235305
VERSION     AX235305.1  GI:15593850
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vider,B.Z. and Katzir,N.
  TITLE     A method that compares genomic sequences
  JOURNAL   Patent: WO 0162967-A 7 30-AUG-2001;
            Genena Ltd. (IL) ; Agricultural Research Organization Newe Ya'Ar
            Research Center (IL)
FEATURES             Location/Qualifiers
     source          1. .13
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ORIGIN

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Qy          8 YYY 10
              |||
Db         11 YYY 13


RESULT 194
AX235305/c
LOCUS       AX235305                  13 bp    DNA     linear   PAT 11-SEP-2001
DEFINITION  Sequence 7 from Patent WO0162967.
ACCESSION   AX235305
VERSION     AX235305.1  GI:15593850
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vider,B.Z. and Katzir,N.
  TITLE     A method that compares genomic sequences
  JOURNAL   Patent: WO 0162967-A 7 30-AUG-2001;
            Genena Ltd. (IL) ; Agricultural Research Organization Newe Ya'Ar
            Research Center (IL)
FEATURES             Location/Qualifiers
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Qy          1 RRR 3
              |||
Db         13 RRR 11


RESULT 195
AR134892
LOCUS       AR134892                  14 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 8 from patent US 6194211.
ACCESSION   AR134892
VERSION     AR134892.1  GI:14123797
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Richards,C.Ann. and Huber,B.
  TITLE     Transcriptional regulatory sequence of carcinoembryonic antigen for
            expression targeting
  JOURNAL   Patent: US 6194211-A 8 27-FEB-2001;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 RRR 3
              |||
Db          1 RRR 3


RESULT 196
AR134892/c
LOCUS       AR134892                  14 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 8 from patent US 6194211.
ACCESSION   AR134892
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VERSION     AR134892.1  GI:14123797
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Richards,C.Ann. and Huber,B.
  TITLE     Transcriptional regulatory sequence of carcinoembryonic antigen for
            expression targeting
  JOURNAL   Patent: US 6194211-A 8 27-FEB-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 14;
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Qy          8 YYY 10
              |||
Db          3 YYY 1


RESULT 197
AR138914
LOCUS       AR138914                  14 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 7 from patent US 6200778.
ACCESSION   AR138914
VERSION     AR138914.1  GI:14481259
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Treco,D.A., Heartlein,M.W. and Selden,R.F.
  TITLE     Genomic sequences for protein production and delivery
  JOURNAL   Patent: US 6200778-A 7 13-MAR-2001;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 198
AR138914/c
LOCUS       AR138914                  14 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 7 from patent US 6200778.
ACCESSION   AR138914
VERSION     AR138914.1  GI:14481259
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Treco,D.A., Heartlein,M.W. and Selden,R.F.
  TITLE     Genomic sequences for protein production and delivery
  JOURNAL   Patent: US 6200778-A 7 13-MAR-2001;
FEATURES             Location/Qualifiers
     source          1. .14
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 199
AR156467
LOCUS       AR156467                  14 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 8 from patent US 6242218.
ACCESSION   AR156467
VERSION     AR156467.1  GI:15125171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Treco,D.A., Heartlein,M.W. and Selden,R.F.
  TITLE     Genomic sequences for protein production and delivery
  JOURNAL   Patent: US 6242218-A 8 05-JUN-2001;
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 200
AR156467/c
LOCUS       AR156467                  14 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 8 from patent US 6242218.
ACCESSION   AR156467
VERSION     AR156467.1  GI:15125171
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Treco,D.A., Heartlein,M.W. and Selden,R.F.
  TITLE     Genomic sequences for protein production and delivery
  JOURNAL   Patent: US 6242218-A 8 05-JUN-2001;
FEATURES             Location/Qualifiers
     source          1. .14
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 6;  Length 14;
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Qy          1 RRR 3
              |||
Db         10 RRR 8


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 15:16:19 ; Search time 386 Seconds
(without alignments)
135.995 Million cell updates/sec

Title: US-09-813-824A-3
Perfect score: 10
Sequence: 1 RRRCWWGYYY 10

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4343386

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 1000 summaries

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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	10	100.0	10	2	AAQ31948	Aaq31948 Monomeric
c	2	10	100.0	10	2	AAQ31948	Aaq31948 Monomeric
	3	10	100.0	10	2	AAV45242	Aav45242 Human ner
c	4	10	100.0	10	2	AAV45242	Aav45242 Human ner
	5	10	100.0	10	2	AAV25510	Aav25510 p53 bindi
c	6	10	100.0	10	2	AAV25510	Aav25510 p53 bindi
	7	10	100.0	10	4	AAF31886	Aaf31886 p53 bindi
c	8	10	100.0	10	4	AAF31886	Aaf31886 p53 bindi
	9	10	100.0	10	4	AAF58009	Aaf58009 Wild-type
c	10	10	100.0	10	4	AAF58009	Aaf58009 Wild-type
	11	10	100.0	10	9	ACA62195	Aca62195 Consensus
c	12	10	100.0	10	9	ACA62195	Aca62195 Consensus
	13	10	100.0	19	6	ABK91337	Abk91337 Human JFY
c	14	10	100.0	19	6	ABK91337	Abk91337 Human JFY
	15	10	100.0	20	3	AAZ51676	Aaz51676 Human p53
c	16	10	100.0	20	3	AAZ51676	Aaz51676 Human p53
	17	10	100.0	20	6	AAL42021	Aal42021 Human gen
c	18	10	100.0	20	6	AAL42021	Aal42021 Human gen
	19	10	100.0	20	6	AAD30357	Aad30357 p53 conse
c	20	10	100.0	20	6	AAD30357	Aad30357 p53 conse
	21	10	100.0	20	10	ADC71586	Adc71586 Degenerat
c	22	10	100.0	20	10	ADC71586	Adc71586 Degenerat
	23	10	100.0	21	3	AAZ51677	Aaz51677 Human p53
c	24	10	100.0	21	3	AAZ51677	Aaz51677 Human p53
	25	5	50.0	20	2	AAQ56429	Aaq56429 E6 consen
c	26	5	50.0	20	2	AAQ56429	Aaq56429 E6 consen
	27	5	50.0	20	2	AAT44825	Aat44825 HPV E6 re
c	28	5	50.0	20	2	AAT44825	Aat44825 HPV E6 re
	29	5	50.0	20	2	AAT77998	Aat77998 Human pap
c	30	5	50.0	20	2	AAT77998	Aat77998 Human pap
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c	32	4	40.0	16	3	ABN87013	Abn87013 Histone m
	33	4	40.0	19	6	ABQ81373	Abq81373 Matrix me
c	34	4	40.0	19	6	ABQ81373	Abq81373 Matrix me
	35	4	40.0	19	6	AAD27333	Aad27333 Human MMP
c	36	4	40.0	19	6	AAD27333	Aad27333 Human MMP
	37	4	40.0	20	2	AAQ56430	Aaq56430 E6 consen
c	38	4	40.0	20	2	AAQ56430	Aaq56430 E6 consen
	39	4	40.0	20	2	AAQ56428	Aaq56428 E6 consen
c	40	4	40.0	20	2	AAQ56428	Aaq56428 E6 consen
	41	4	40.0	20	2	AAT44824	Aat44824 HPV E6 re
c	42	4	40.0	20	2	AAT44824	Aat44824 HPV E6 re
	43	4	40.0	20	2	AAT44826	Aat44826 HPV E6 re
c	44	4	40.0	20	2	AAT44826	Aat44826 HPV E6 re
	45	4	40.0	20	2	AAT77997	Aat77997 Human pap
c	46	4	40.0	20	2	AAT77997	Aat77997 Human pap
	47	4	40.0	20	2	AAT77999	Aat77999 Human pap
c	48	4	40.0	20	2	AAT77999	Aat77999 Human pap
	49	4	40.0	20	2	AAV10231	Aav10231 p53 bindi
c	50	4	40.0	20	2	AAV10231	Aav10231 p53 bindi
	51	4	40.0	20	10	ADF44299	Adf44299 HPV PCR p
c	52	4	40.0	20	10	ADF44299	Adf44299 HPV PCR p
	53	4	40.0	21	4	AAH44952	Aah44952 HIV Gp41
c	54	4	40.0	21	4	AAH44952	Aah44952 HIV Gp41
	55	4	40.0	25	9	ADA50047	Ada50047 Pig cDNA
c	56	4	40.0	25	9	ADA50047	Ada50047 Pig cDNA
	57	4	40.0	26	3	AAZ57335	Aaz57335 TRH-produ
c	58	4	40.0	26	3	AAZ57335	Aaz57335 TRH-produ
	59	4	40.0	27	2	AAQ24776	Aaq24776 Arbitrary
c	60	4	40.0	27	2	AAQ24776	Aaq24776 Arbitrary
	61	4	40.0	27	2	AAT16364	Aat16364 AP-PCR Kp
c	62	4	40.0	27	2	AAT16364	Aat16364 AP-PCR Kp
	63	4	40.0	27	3	AAZ40324	Aaz40324 PCR prime
c	64	4	40.0	27	3	AAZ40324	Aaz40324 PCR prime
	65	4	40.0	27	4	AAS04151	Aas04151 Degenerat
c	66	4	40.0	27	4	AAS04151	Aas04151 Degenerat
	67	4	40.0	27	12	ADJ63790	Adj63790 Primer #2
c	68	4	40.0	27	12	ADJ63790	Adj63790 Primer #2
	69	4	40.0	27	12	ADJ63791	Adj63791 Primer fo
c	70	4	40.0	27	12	ADJ63791	Adj63791 Primer fo
	71	4	40.0	30	6	AAD46919	Aad46919 Histone 3
c	72	4	40.0	30	6	AAD46919	Aad46919 Histone 3
	73	4	40.0	30	6	AAD46937	Aad46937 Histone 3
c	74	4	40.0	30	6	AAD46937	Aad46937 Histone 3
	75	4	40.0	32	2	AAQ30066	Aaq30066 Sequence
c	76	4	40.0	32	2	AAQ30066	Aaq30066 Sequence
	77	4	40.0	38	2	AAV39802	Aav39802 Oligonucl
c	78	4	40.0	38	2	AAV39802	Aav39802 Oligonucl
	79	3	30.0	6	3	AAA28440	Aaa28440 Synthetic
c	80	3	30.0	6	3	AAA28440	Aaa28440 Synthetic
	81	3	30.0	6	12	ADF42928	Adf42928 Methylate
c	82	3	30.0	6	12	ADF42928	Adf42928 Methylate
	83	3	30.0	6	12	ADL35954	Adl35954 Non-methy
c	84	3	30.0	6	12	ADL35954	Adl35954 Non-methy
	85	3	30.0	7	3	AAZ88744	Aaz88744 V. choler
c	86	3	30.0	7	3	AAZ88744	Aaz88744 V. choler
	87	3	30.0	8	3	AAZ88743	Aaz88743 V. choler
c	88	3	30.0	8	3	AAZ88743	Aaz88743 V. choler
	89	3	30.0	8	3	AAA28439	Aaa28439 Synthetic
c	90	3	30.0	8	3	AAA28439	Aaa28439 Synthetic
	91	3	30.0	9	2	AAQ63868	Aaq63868 Haematopo
c	92	3	30.0	9	2	AAQ63868	Aaq63868 Haematopo
	93	3	30.0	9	2	AAT96075	Aat96075 Recombina
c	94	3	30.0	9	2	AAT96075	Aat96075 Recombina

95	3	30.0	10	2	AAQ31609	Aaq31609 Cauliflow
c 96	3	30.0	10	2	AAQ31609	Aaq31609 Cauliflow
97	3	30.0	10	2	AAQ30505	Aaq30505 Serum res
c 98	3	30.0	10	2	AAQ30505	Aaq30505 Serum res
99	3	30.0	10	2	AAQ38817	Aaq38817 CaMV 35S
c 100	3	30.0	10	2	AAQ38817	Aaq38817 CaMV 35S
101	3	30.0	10	2	AAQ72970	Aaq72970 Engineere
c 102	3	30.0	10	2	AAQ72970	Aaq72970 Engineere
103	3	30.0	10	2	AAQ81756	Aaq81756 CaMV 35S
c 104	3	30.0	10	2	AAQ81756	Aaq81756 CaMV 35S
105	3	30.0	10	2	AAT96065	Aat96065 Recombina
c 106	3	30.0	10	2	AAT96065	Aat96065 Recombina
107	3	30.0	10	2	AAT96076	Aat96076 Recombina
c 108	3	30.0	10	2	AAT96076	Aat96076 Recombina
109	3	30.0	10	2	AAX88060	Aax88060 Serum res
c 110	3	30.0	10	2	AAX88060	Aax88060 Serum res
111	3	30.0	10	3	AAA91882	Aaa91882 Complemen
c 112	3	30.0	10	3	AAA91882	Aaa91882 Complemen
113	3	30.0	10	3	AAA16552	Aaa16552 Initiator
c 114	3	30.0	10	3	AAA16552	Aaa16552 Initiator
115	3	30.0	10	3	AAA52471	Aaa52471 Initiator
c 116	3	30.0	10	3	AAA52471	Aaa52471 Initiator
117	3	30.0	10	4	AAH26710	Aah26710 CArG box
c 118	3	30.0	10	4	AAH26710	Aah26710 CArG box
119	3	30.0	10	4	AAD20602	Aad20602 Consensus
c 120	3	30.0	10	4	AAD20602	Aad20602 Consensus
121	3	30.0	10	4	AAD21142	Aad21142 Consensus
c 122	3	30.0	10	4	AAD21142	Aad21142 Consensus
123	3	30.0	10	5	AAD04664	Aad04664 Thermus 9
c 124	3	30.0	10	5	AAD04664	Aad04664 Thermus 9
125	3	30.0	10	6	ABK33367	Abk33367 SRF bindi
c 126	3	30.0	10	6	ABK33367	Abk33367 SRF bindi
127	3	30.0	10	6	ABK85627	Abk85627 Serum res
c 128	3	30.0	10	6	ABK85627	Abk85627 Serum res
129	3	30.0	10	6	ABL53549	Abl53549 CpG motif
c 130	3	30.0	10	6	ABL53549	Abl53549 CpG motif
131	3	30.0	10	6	ADG88268	Adg88268 Pathogen
c 132	3	30.0	10	6	ADG88268	Adg88268 Pathogen
133	3	30.0	10	8	ABZ24785	Abz24785 Oligodeox
c 134	3	30.0	10	8	ABZ24785	Abz24785 Oligodeox
135	3	30.0	10	12	ADJ56890	Adj56890 Antioxida
c 136	3	30.0	10	12	ADJ56890	Adj56890 Antioxida
137	3	30.0	10	12	ADN98340	Adn98340 Serum res
c 138	3	30.0	10	12	ADN98340	Adn98340 Serum res
139	3	30.0	11	2	AAT96077	Aat96077 Recombina
c 140	3	30.0	11	2	AAT96077	Aat96077 Recombina
141	3	30.0	11	6	ABA94933	Aba94933 Human ecN
c 142	3	30.0	11	6	ABA94933	Aba94933 Human ecN
143	3	30.0	11	10	ADJ71749	Adj71749 Aptamer p
c 144	3	30.0	11	10	ADJ71749	Adj71749 Aptamer p
145	3	30.0	12	2	AAT04535	Aat04535 Oxygen de
c 146	3	30.0	12	2	AAT04535	Aat04535 Oxygen de
147	3	30.0	12	2	AAT96066	Aat96066 Recombina
c 148	3	30.0	12	2	AAT96066	Aat96066 Recombina
149	3	30.0	12	2	AAT96078	Aat96078 Recombina
c 150	3	30.0	12	2	AAT96078	Aat96078 Recombina
151	3	30.0	12	6	ADG88255	Adg88255 Pathogen
c 152	3	30.0	12	6	ADG88255	Adg88255 Pathogen
153	3	30.0	12	10	ADB81333	Adb81333 Bacteriop
c 154	3	30.0	12	10	ADB81333	Adb81333 Bacteriop
155	3	30.0	12	10	ADB81334	Adb81334 Bacteriop
c 156	3	30.0	12	10	ADB81334	Adb81334 Bacteriop
157	3	30.0	13	2	AAT96067	Aat96067 Recombina
c 158	3	30.0	13	2	AAT96067	Aat96067 Recombina
159	3	30.0	13	2	AAT96079	Aat96079 Recombina
c 160	3	30.0	13	2	AAT96079	Aat96079 Recombina
161	3	30.0	13	6	ABL42250	Abl42250 Animal ci
c 162	3	30.0	13	6	ABL42250	Abl42250 Animal ci
163	3	30.0	13	11	ADL71828	Adl71828 Anticance
c 164	3	30.0	13	11	ADL71828	Adl71828 Anticance
165	3	30.0	13	12	ACC85667	Acc85667 RNA ligan
c 166	3	30.0	13	12	ACC85667	Acc85667 RNA ligan
167	3	30.0	14	2	AAQ80951	Aaq80951 HIV prote
c 168	3	30.0	14	2	AAQ80951	Aaq80951 HIV prote
169	3	30.0	14	2	AAQ80974	Aaq80974 HIV prote
c 170	3	30.0	14	2	AAQ80974	Aaq80974 HIV prote
171	3	30.0	14	2	AAT96068	Aat96068 Recombina
c 172	3	30.0	14	2	AAT96068	Aat96068 Recombina
173	3	30.0	14	2	AAT96080	Aat96080 Recombina
c 174	3	30.0	14	2	AAT96080	Aat96080 Recombina
175	3	30.0	14	2	AAV22311	Aav22311 ISRE gene
c 176	3	30.0	14	2	AAV22311	Aav22311 ISRE gene
177	3	30.0	14	2	AAV22312	Aav22312 ISRE comp
c 178	3	30.0	14	2	AAV22312	Aav22312 ISRE comp
179	3	30.0	14	3	AAZ43723	Aaz43723 Human FSH
c 180	3	30.0	14	3	AAZ43723	Aaz43723 Human FSH
181	3	30.0	14	3	AAA91879	Aaa91879 Complemen
c 182	3	30.0	14	3	AAA91879	Aaa91879 Complemen
183	3	30.0	14	4	AAD17448	Aad17448 Splice ac
c 184	3	30.0	14	4	AAD17448	Aad17448 Splice ac
185	3	30.0	14	6	ABA99069	Aba99069 Gut-enric
c 186	3	30.0	14	6	ABA99069	Aba99069 Gut-enric
187	3	30.0	14	12	ADF83663	Adf83663 Pravastat
c 188	3	30.0	14	12	ADF83663	Adf83663 Pravastat
189	3	30.0	15	2	AAT96081	Aat96081 Recombina
c 190	3	30.0	15	2	AAT96081	Aat96081 Recombina
191	3	30.0	15	2	AAT96069	Aat96069 Recombina
c 192	3	30.0	15	2	AAT96069	Aat96069 Recombina
193	3	30.0	15	5	AAF75852	Aaf75852 3' splice
c 194	3	30.0	15	5	AAF75852	Aaf75852 3' splice
195	3	30.0	15	10	ADF29171	Adf29171 Beta-glob
c 196	3	30.0	15	10	ADF29171	Adf29171 Beta-glob
197	3	30.0	15	10	ADF29180	Adf29180 Binding o
c 198	3	30.0	15	10	ADF29180	Adf29180 Binding o
199	3	30.0	15	10	ADJ71750	Adj71750 Aptamer p
c 200	3	30.0	15	10	ADJ71750	Adj71750 Aptamer p
201	3	30.0	15	10	ADJ72504	Adj72504 Human GP1
c 202	3	30.0	15	10	ADJ72504	Adj72504 Human GP1
203	3	30.0	15	10	ADJ72486	Adj72486 Human GP1
c 204	3	30.0	15	10	ADJ72486	Adj72486 Human GP1
205	3	30.0	16	2	AAQ50544	Aaq50544 Probe cCI
c 206	3	30.0	16	2	AAQ50544	Aaq50544 Probe cCI
207	3	30.0	16	2	AAQ43200	Aaq43200 Splice ac
c 208	3	30.0	16	2	AAQ43200	Aaq43200 Splice ac
209	3	30.0	16	2	AAT96070	Aat96070 Recombina
c 210	3	30.0	16	2	AAT96070	Aat96070 Recombina
211	3	30.0	16	2	AAT96082	Aat96082 Recombina
c 212	3	30.0	16	2	AAT96082	Aat96082 Recombina
213	3	30.0	16	2	AAX04104	Aax04104 PUR eleme
c 214	3	30.0	16	2	AAX04104	Aax04104 PUR eleme
215	3	30.0	16	2	AAX55934	Aax55934 Inference
c 216	3	30.0	16	2	AAX55934	Aax55934 Inference
217	3	30.0	16	2	AAX55931	Aax55931 Inference
c 218	3	30.0	16	2	AAX55931	Aax55931 Inference
219	3	30.0	16	2	AAX55936	Aax55936 Inference
c 220	3	30.0	16	2	AAX55936	Aax55936 Inference
221	3	30.0	16	2	AAX55946	Aax55946 Inference
c 222	3	30.0	16	2	AAX55946	Aax55946 Inference
223	3	30.0	16	2	AAX55945	Aax55945 Inference
c 224	3	30.0	16	2	AAX55945	Aax55945 Inference
225	3	30.0	16	2	AAX55930	Aax55930 Inference
c 226	3	30.0	16	2	AAX55930	Aax55930 Inference
227	3	30.0	16	2	AAX55940	Aax55940 Inference
c 228	3	30.0	16	2	AAX55940	Aax55940 Inference
229	3	30.0	16	2	AAX55935	Aax55935 Inference
c 230	3	30.0	16	2	AAX55935	Aax55935 Inference
231	3	30.0	16	2	AAX55937	Aax55937 Inference
c 232	3	30.0	16	2	AAX55937	Aax55937 Inference
233	3	30.0	16	2	AAX55939	Aax55939 Inference
c 234	3	30.0	16	2	AAX55939	Aax55939 Inference
235	3	30.0	16	2	AAZ40420	Aaz40420 Consensus
c 236	3	30.0	16	2	AAZ40420	Aaz40420 Consensus
237	3	30.0	16	4	AAA89362	Aaa89362 Arabidops
c 238	3	30.0	16	4	AAA89362	Aaa89362 Arabidops
239	3	30.0	16	4	AAI70031	Aai70031 AG domain
c 240	3	30.0	16	4	AAI70031	Aai70031 AG domain

	241	3	30.0	16	4	AAI70032 Aai70032 AG domain
c	242	3	30.0	16	4	AAI70032 Aai70032 AG domain
	243	3	30.0	17	1	AAN70947 Aan70947 Sequence
c	244	3	30.0	17	1	AAN70947 Aan70947 Sequence
	245	3	30.0	17	2	AAQ55881 Aaq55881 Oligonucl
c	246	3	30.0	17	2	AAQ55881 Aaq55881 Oligonucl
	247	3	30.0	17	2	AAT12327 Aat12327 DNA prime
c	248	3	30.0	17	2	AAT12327 Aat12327 DNA prime
	249	3	30.0	17	2	AAT66830 Aat66830 Herpes si
c	250	3	30.0	17	2	AAT66830 Aat66830 Herpes si
	251	3	30.0	17	2	AAT96083 Aat96083 Recombina
c	252	3	30.0	17	2	AAT96083 Aat96083 Recombina
	253	3	30.0	17	2	AAT96071 Aat96071 Recombina
c	254	3	30.0	17	2	AAT96071 Aat96071 Recombina
	255	3	30.0	17	2	AAV28595 Aav28595 Murine mo
c	256	3	30.0	17	2	AAV28595 Aav28595 Murine mo
	257	3	30.0	17	2	AAV28594 Aav28594 Murine mo
c	258	3	30.0	17	2	AAV28594 Aav28594 Murine mo
	259	3	30.0	17	2	AAV63282 Aav63282 PCR prime
c	260	3	30.0	17	2	AAV63282 Aav63282 PCR prime
	261	3	30.0	17	2	AAZ07346 Aaz07346 Cystine k
c	262	3	30.0	17	2	AAZ07346 Aaz07346 Cystine k
	263	3	30.0	17	2	AAX32728 Aax32728 Recogniti
c	264	3	30.0	17	2	AAX32728 Aax32728 Recogniti
	265	3	30.0	17	3	AAD00226 Aad00226 PCR prime
c	266	3	30.0	17	3	AAD00226 Aad00226 PCR prime
	267	3	30.0	17	3	AAA51503 Aaa51503 Degenerat
c	268	3	30.0	17	3	AAA51503 Aaa51503 Degenerat
	269	3	30.0	17	3	AAC81560 Aac81560 Human zve
c	270	3	30.0	17	3	AAC81560 Aac81560 Human zve
	271	3	30.0	17	4	AAF74549 Aaf74549 Aspergill
c	272	3	30.0	17	4	AAF74549 Aaf74549 Aspergill
	273	3	30.0	17	6	AAS16772 Aas16772 Polyketid
c	274	3	30.0	17	6	AAS16772 Aas16772 Polyketid
	275	3	30.0	17	6	AAD42086 Aad42086 Bovine PA
c	276	3	30.0	17	6	AAD42086 Aad42086 Bovine PA
	277	3	30.0	17	6	ABS68617 Abs68617 Human zve
c	278	3	30.0	17	6	ABS68617 Abs68617 Human zve
	279	3	30.0	17	6	ABA98489 Aba98489 Corynebac
c	280	3	30.0	17	6	ABA98489 Aba98489 Corynebac
	281	3	30.0	17	6	ABK14936 Abk14936 Bovine (P
c	282	3	30.0	17	6	ABK14936 Abk14936 Bovine (P
	283	3	30.0	17	6	ABK14498 Abk14498 Bovine PA
c	284	3	30.0	17	6	ABK14498 Abk14498 Bovine PA
	285	3	30.0	17	8	ABX14482 Abx14482 Degenerat
c	286	3	30.0	17	8	ABX14482 Abx14482 Degenerat
	287	3	30.0	17	8	ABX93151 Abx93151 Degenerat
c	288	3	30.0	17	8	ABX93151 Abx93151 Degenerat
	289	3	30.0	17	10	AAD61056 Aad61056 Human zsi
c	290	3	30.0	17	10	AAD61056 Aad61056 Human zsi
	291	3	30.0	17	10	ADF72000 Adf72000 Zsig51 cD
c	292	3	30.0	17	10	ADF72000 Adf72000 Zsig51 cD
	293	3	30.0	17	10	ADG47719 Adg47719 zvegf3 de
c	294	3	30.0	17	10	ADG47719 Adg47719 zvegf3 de
	295	3	30.0	17	10	ADH89090 Adh89090 Degenerat
c	296	3	30.0	17	10	ADH89090 Adh89090 Degenerat
	297	3	30.0	17	10	ACA64114 Aca64114 ZVEGF4 de
c	298	3	30.0	17	10	ACA64114 Aca64114 ZVEGF4 de
	299	3	30.0	17	12	ADJ32763 Adj32763 Growth fa
c	300	3	30.0	17	12	ADJ32763 Adj32763 Growth fa
	301	3	30.0	18	2	AAT96084 Aat96084 Recombina
c	302	3	30.0	18	2	AAT96084 Aat96084 Recombina
	303	3	30.0	18	2	AAT96072 Aat96072 Recombina
c	304	3	30.0	18	2	AAT96072 Aat96072 Recombina
	305	3	30.0	18	2	AAX86618 Aax86618 Probe for
c	306	3	30.0	18	2	AAX86618 Aax86618 Probe for
	307	3	30.0	18	5	AAF77388 Aaf77388 PCR prime
c	308	3	30.0	18	5	AAF77388 Aaf77388 PCR prime
	309	3	30.0	18	6	AAL45229 Aal45229 Human pap
c	310	3	30.0	18	6	AAL45229 Aal45229 Human pap
	311	3	30.0	18	8	ACC57884 Acc57884 DNA fragm
c	312	3	30.0	18	8	ACC57884 Acc57884 DNA fragm
	313	3	30.0	18	10	ADF43078 Adf43078 Desulfovi
c	314	3	30.0	18	10	ADF43078 Adf43078 Desulfovi
	315	3	30.0	18	10	ADF93163 Adf93163 Consensus
c	316	3	30.0	18	10	ADF93163 Adf93163 Consensus
	317	3	30.0	18	12	ADN96890 Adn96890 Immunosti
c	318	3	30.0	18	12	ADN96890 Adn96890 Immunosti
	319	3	30.0	19	2	AAQ56437 Aaq56437 E6 consen
c	320	3	30.0	19	2	AAQ56437 Aaq56437 E6 consen
	321	3	30.0	19	2	AAQ55880 Aaq55880 Oligonucl
c	322	3	30.0	19	2	AAQ55880 Aaq55880 Oligonucl
	323	3	30.0	19	2	AAT44835 Aat44835 HPV E6 re
c	324	3	30.0	19	2	AAT44835 Aat44835 HPV E6 re
	325	3	30.0	19	2	AAT78000 Aat78000 Human pap
c	326	3	30.0	19	2	AAT78000 Aat78000 Human pap
	327	3	30.0	19	2	AAT66829 Aat66829 Herpes si
c	328	3	30.0	19	2	AAT66829 Aat66829 Herpes si
	329	3	30.0	19	2	AAT96073 Aat96073 Recombina
c	330	3	30.0	19	2	AAT96073 Aat96073 Recombina
	331	3	30.0	19	2	AAV17433 Aav17433 Probe WD6
c	332	3	30.0	19	2	AAV17433 Aav17433 Probe WD6
	333	3	30.0	19	3	AAZ46180 Aaz46180 Ribozyme
c	334	3	30.0	19	3	AAZ46180 Aaz46180 Ribozyme
	335	3	30.0	19	6	AAD37969 Aad37969 RNA bindi
c	336	3	30.0	19	6	AAD37969 Aad37969 RNA bindi
	337	3	30.0	19	12	ADM16445 Adm16445 RNA intro
c	338	3	30.0	19	12	ADM16445 Adm16445 RNA intro
	339	3	30.0	19	12	ADN96891 Adn96891 Immunosti
c	340	3	30.0	19	12	ADN96891 Adn96891 Immunosti
	341	3	30.0	19	12	ADN96901 Adn96901 Immunosti
c	342	3	30.0	19	12	ADN96901 Adn96901 Immunosti
	343	3	30.0	20	2	AAQ37771 Aaq37771 HCV unive
c	344	3	30.0	20	2	AAQ37771 Aaq37771 HCV unive
	345	3	30.0	20	2	AAQ37769 Aaq37769 HCV unive
c	346	3	30.0	20	2	AAQ37769 Aaq37769 HCV unive
	347	3	30.0	20	2	AAQ56425 Aaq56425 E6 consen
c	348	3	30.0	20	2	AAQ56425 Aaq56425 E6 consen
	349	3	30.0	20	2	AAQ80806 Aaq80806 HCV genot
c	350	3	30.0	20	2	AAQ80806 Aaq80806 HCV genot
	351	3	30.0	20	2	AAQ80804 Aaq80804 HCV genot
c	352	3	30.0	20	2	AAQ80804 Aaq80804 HCV genot
	353	3	30.0	20	2	AAT30076 Aat30076 Blowfly P
c	354	3	30.0	20	2	AAT30076 Aat30076 Blowfly P
	355	3	30.0	20	2	AAT36505 Aat36505 Primer DN
c	356	3	30.0	20	2	AAT36505 Aat36505 Primer DN
	357	3	30.0	20	2	AAT44821 Aat44821 HPV E6 re
c	358	3	30.0	20	2	AAT44821 Aat44821 HPV E6 re
	359	3	30.0	20	2	AAT89906 Aat89906 Human ubi
c	360	3	30.0	20	2	AAT89906 Aat89906 Human ubi
	361	3	30.0	20	2	AAT79629 Aat79629 Human Doc
c	362	3	30.0	20	2	AAT79629 Aat79629 Human Doc
	363	3	30.0	20	2	AAT51573 Aat51573 Herpes vi
c	364	3	30.0	20	2	AAT51573 Aat51573 Herpes vi
	365	3	30.0	20	2	AAT77994 Aat77994 Human pap
c	366	3	30.0	20	2	AAT77994 Aat77994 Human pap
	367	3	30.0	20	2	AAT89691 Aat89691 PCR prime
c	368	3	30.0	20	2	AAT89691 Aat89691 PCR prime
	369	3	30.0	20	2	AAT96074 Aat96074 Recombina
c	370	3	30.0	20	2	AAT96074 Aat96074 Recombina
	371	3	30.0	20	2	AAV17457 Aav17457 Primer WD
c	372	3	30.0	20	2	AAV17457 Aav17457 Primer WD
	373	3	30.0	20	2	AAX32730 Aax32730 Recogniti
c	374	3	30.0	20	2	AAX32730 Aax32730 Recogniti
	375	3	30.0	20	3	AAZ34806 Aaz34806 Cat CD86
c	376	3	30.0	20	3	AAZ34806 Aaz34806 Cat CD86
	377	3	30.0	20	3	AAZ34858 Aaz34858 Feline CD
c	378	3	30.0	20	3	AAZ34858 Aaz34858 Feline CD
	379	3	30.0	20	4	AAC85502 Aac85502 Primer #1
c	380	3	30.0	20	4	AAC85502 Aac85502 Primer #1
	381	3	30.0	20	4	AAH22881 Aah22881 R. ruber
c	382	3	30.0	20	4	AAH22881 Aah22881 R. ruber
	383	3	30.0	20	4	AAH00945 Aah00945 Universal
c	384	3	30.0	20	4	AAH00945 Aah00945 Universal
	385	3	30.0	20	4	AAF79961 Aaf79961 PCR prime
c	386	3	30.0	20	4	AAF79961 Aaf79961 PCR prime

387	3	30.0	20	4	AAD18493	Aad18493	A. oryzae
c 388	3	30.0	20	4	AAD18493	Aad18493	A. oryzae
389	3	30.0	20	5	AAF26152	Aaf26152	C. nassat
c 390	3	30.0	20	5	AAF26152	Aaf26152	C. nassat
391	3	30.0	20	5	AAF26153	Aaf26153	C. nassat
c 392	3	30.0	20	5	AAF26153	Aaf26153	C. nassat
393	3	30.0	20	6	ABK85599	Abk85599	Splice ac
c 394	3	30.0	20	6	ABK85599	Abk85599	Splice ac
395	3	30.0	20	6	ABK67569	Abk67569	Feline CD
c 396	3	30.0	20	6	ABK67569	Abk67569	Feline CD
397	3	30.0	20	8	ACC79624	Acc79624	Prostagla
c 398	3	30.0	20	8	ACC79624	Acc79624	Prostagla
399	3	30.0	20	8	ABX15801	Abx15801	Splice ac
c 400	3	30.0	20	8	ABX15801	Abx15801	Splice ac
401	3	30.0	20	8	ABA00905	Aba00905	LOX-1 gen
c 402	3	30.0	20	8	ABA00905	Aba00905	LOX-1 gen
403	3	30.0	20	10	ADH11547	Adh11547	Prostagla
c 404	3	30.0	20	10	ADH11547	Adh11547	Prostagla
405	3	30.0	20	12	ADP03267	Adp03267	Primer 2
c 406	3	30.0	20	12	ADP03267	Adp03267	Primer 2
407	3	30.0	20	12	ADO43712	Ado43712	Consensus
c 408	3	30.0	20	12	ADO43712	Ado43712	Consensus
409	3	30.0	20	12	ADN96902	Adn96902	Immunosti
c 410	3	30.0	20	12	ADN96902	Adn96902	Immunosti
411	3	30.0	20	12	ADN96912	Adn96912	Immunosti
c 412	3	30.0	20	12	ADN96912	Adn96912	Immunosti
413	3	30.0	20	12	ADN96892	Adn96892	Immunosti
c 414	3	30.0	20	12	ADN96892	Adn96892	Immunosti
415	3	30.0	20	12	ADN96967	Adn96967	Immunosti
c 416	3	30.0	20	12	ADN96967	Adn96967	Immunosti
417	3	30.0	20	12	ADQ07344	Adq07344	Paraxanth
c 418	3	30.0	20	12	ADQ07344	Adq07344	Paraxanth
419	3	30.0	21	2	AAQ56418	Aaq56418	E7 consen
c 420	3	30.0	21	2	AAQ56418	Aaq56418	E7 consen
421	3	30.0	21	2	AAT44820	Aat44820	HPV E7 re
c 422	3	30.0	21	2	AAT44820	Aat44820	HPV E7 re
423	3	30.0	21	2	AAT84920	Aat84920	Human nit
c 424	3	30.0	21	2	AAT84920	Aat84920	Human nit
425	3	30.0	21	2	AAT78162	Aat78162	Human pap
c 426	3	30.0	21	2	AAT78162	Aat78162	Human pap
427	3	30.0	21	2	AAV17454	Aav17454	Primer WD
c 428	3	30.0	21	2	AAV17454	Aav17454	Primer WD
429	3	30.0	21	2	AAV54509	Aav54509	Nucleotid
c 430	3	30.0	21	2	AAV54509	Aav54509	Nucleotid
431	3	30.0	21	2	AAV54542	Aav54542	Nucleotid
c 432	3	30.0	21	2	AAV54542	Aav54542	Nucleotid
433	3	30.0	21	2	AAV54511	Aav54511	Nucleotid
c 434	3	30.0	21	2	AAV54511	Aav54511	Nucleotid
435	3	30.0	21	2	AAV54540	Aav54540	Nucleotid
c 436	3	30.0	21	2	AAV54540	Aav54540	Nucleotid
437	3	30.0	21	2	AAX27509	Aax27509	Banana AC
c 438	3	30.0	21	2	AAX27509	Aax27509	Banana AC
439	3	30.0	21	3	AAZ93337	Aaz93337	Primer us
c 440	3	30.0	21	3	AAZ93337	Aaz93337	Primer us
441	3	30.0	21	4	AAS09909	Aas09909	PCR prime
c 442	3	30.0	21	4	AAS09909	Aas09909	PCR prime
443	3	30.0	21	4	AAH44950	Aah44950	HIV Gp41
c 444	3	30.0	21	4	AAH44950	Aah44950	HIV Gp41
445	3	30.0	21	4	AAD03852	Aad03852	Human cel
c 446	3	30.0	21	4	AAD03852	Aad03852	Human cel
447	3	30.0	21	4	AAS00685	Aas00685	Forward P
c 448	3	30.0	21	4	AAS00685	Aas00685	Forward P
449	3	30.0	21	5	AAF75861	Aaf75861	PCR prime
c 450	3	30.0	21	5	AAF75861	Aaf75861	PCR prime
451	3	30.0	21	6	AAS18423	Aas18423	Degenerat
c 452	3	30.0	21	6	AAS18423	Aas18423	Degenerat
453	3	30.0	21	8	ABX16353	Abx16353	Human che
c 454	3	30.0	21	8	ABX16353	Abx16353	Human che
455	3	30.0	21	8	ABZ69389	Abz69389	MDS assoc
c 456	3	30.0	21	8	ABZ69389	Abz69389	MDS assoc
457	3	30.0	21	10	ADC72202	Adc72202	Human ste
c 458	3	30.0	21	10	ADC72202	Adc72202	Human ste
459	3	30.0	21	10	ADC72204	Adc72204	Human ste
c 460	3	30.0	21	10	ADC72204	Adc72204	Human ste
461	3	30.0	21	10	ADC72194	Adc72194	Human ste
c 462	3	30.0	21	10	ADC72194	Adc72194	Human ste
463	3	30.0	21	10	ADJ72442	Adj72442	Human GP1
c 464	3	30.0	21	10	ADJ72442	Adj72442	Human GP1
465	3	30.0	21	11	ADL91011	Adl91011	Pig CTLA4
c 466	3	30.0	21	11	ADL91011	Adl91011	Pig CTLA4
467	3	30.0	21	12	ADG77097	Adg77097	V-gene pr
c 468	3	30.0	21	12	ADG77097	Adg77097	V-gene pr
469	3	30.0	21	12	ADO58044	Ado58044	B cell VH
c 470	3	30.0	21	12	ADO58044	Ado58044	B cell VH
471	3	30.0	21	12	ADN96923	Adn96923	Immunosti
c 472	3	30.0	21	12	ADN96923	Adn96923	Immunosti
473	3	30.0	21	12	ADN96978	Adn96978	Immunosti
c 474	3	30.0	21	12	ADN96978	Adn96978	Immunosti
475	3	30.0	21	12	ADN96968	Adn96968	Immunosti
c 476	3	30.0	21	12	ADN96968	Adn96968	Immunosti
477	3	30.0	21	12	ADN96893	Adn96893	Immunosti
c 478	3	30.0	21	12	ADN96893	Adn96893	Immunosti
479	3	30.0	21	12	ADN96903	Adn96903	Immunosti
c 480	3	30.0	21	12	ADN96903	Adn96903	Immunosti
481	3	30.0	21	12	ADN96913	Adn96913	Immunosti
c 482	3	30.0	21	12	ADN96913	Adn96913	Immunosti
483	3	30.0	22	2	AAT91261	Aat91261	GBV hepat
c 484	3	30.0	22	2	AAT91261	Aat91261	GBV hepat
485	3	30.0	22	2	AAX60956	Aax60956	Hepatitis
c 486	3	30.0	22	2	AAX60956	Aax60956	Hepatitis
487	3	30.0	22	3	AAZ91067	Aaz91067	Primer 3P
c 488	3	30.0	22	3	AAZ91067	Aaz91067	Primer 3P
489	3	30.0	22	4	ABN80688	Abn80688	Bacteral
c 490	3	30.0	22	4	ABN80688	Abn80688	Bacteral
491	3	30.0	22	4	AAD18781	Aad18781	PCR prime
c 492	3	30.0	22	4	AAD18781	Aad18781	PCR prime
493	3	30.0	22	12	ADN96934	Adn96934	Immunosti
c 494	3	30.0	22	12	ADN96934	Adn96934	Immunosti
495	3	30.0	22	12	ADN96894	Adn96894	Immunosti
c 496	3	30.0	22	12	ADN96894	Adn96894	Immunosti
497	3	30.0	22	12	ADN96904	Adn96904	Immunosti
c 498	3	30.0	22	12	ADN96904	Adn96904	Immunosti
499	3	30.0	22	12	ADN96914	Adn96914	Immunosti
c 500	3	30.0	22	12	ADN96914	Adn96914	Immunosti
501	3	30.0	22	12	ADN96979	Adn96979	Immunosti
c 502	3	30.0	22	12	ADN96979	Adn96979	Immunosti
503	3	30.0	22	12	ADN96924	Adn96924	Immunosti
c 504	3	30.0	22	12	ADN96924	Adn96924	Immunosti
505	3	30.0	22	12	ADN96989	Adn96989	Immunosti
c 506	3	30.0	22	12	ADN96989	Adn96989	Immunosti
507	3	30.0	22	12	ADN96969	Adn96969	Immunosti
c 508	3	30.0	22	12	ADN96969	Adn96969	Immunosti
509	3	30.0	23	2	AAQ12286	Aaq12286	Probe A f
c 510	3	30.0	23	2	AAQ12286	Aaq12286	Probe A f
511	3	30.0	23	2	AAQ12582	Aaq12582	Morpholin
c 512	3	30.0	23	2	AAQ12582	Aaq12582	Morpholin
513	3	30.0	23	2	AAQ68390	Aaq68390	CGL prime
c 514	3	30.0	23	2	AAQ68390	Aaq68390	CGL prime
515	3	30.0	23	2	AAV54495	Aav54495	Nucleotid
c 516	3	30.0	23	2	AAV54495	Aav54495	Nucleotid
517	3	30.0	23	2	AAV54460	Aav54460	Nucleotid
c 518	3	30.0	23	2	AAV54460	Aav54460	Nucleotid
519	3	30.0	23	2	AAV54497	Aav54497	Nucleotid
c 520	3	30.0	23	2	AAV54497	Aav54497	Nucleotid
521	3	30.0	23	2	AAZ00250	Aaz00250	HEV US-2
c 522	3	30.0	23	2	AAZ00250	Aaz00250	HEV US-2
523	3	30.0	23	2	AAX15289	Aax15289	PCR prime
c 524	3	30.0	23	2	AAX15289	Aax15289	PCR prime
525	3	30.0	23	3	AAA40003	Aaa40003	Rice dise
c 526	3	30.0	23	3	AAA40003	Aaa40003	Rice dise
527	3	30.0	23	4	AAD19026	Aad19026	Hepatitis
c 528	3	30.0	23	4	AAD19026	Aad19026	Hepatitis
529	3	30.0	23	4	AAF69867	Aaf69867	Human TNF
c 530	3	30.0	23	4	AAF69867	Aaf69867	Human TNF
531	3	30.0	23	4	AAF69865	Aaf69865	Human TNF
c 532	3	30.0	23	4	AAF69865	Aaf69865	Human TNF

	533	3	30.0	23	4	AAI69639 Aai69639 Hepatitis
c	534	3	30.0	23	4	AAI69639 Aai69639 Hepatitis
	535	3	30.0	23	4	AAI69642 Aai69642 Hepatitis
c	536	3	30.0	23	4	AAI69642 Aai69642 Hepatitis
	537	3	30.0	23	5	AAF62310 Aaf62310 Human cyc
c	538	3	30.0	23	5	AAF62310 Aaf62310 Human cyc
	539	3	30.0	23	6	ABA02781 Aba02781 Degranula
c	540	3	30.0	23	6	ABA02781 Aba02781 Degranula
	541	3	30.0	23	6	AAD32969 Aad32969 Pear poly
c	542	3	30.0	23	6	AAD32969 Aad32969 Pear poly
	543	3	30.0	23	6	ABN86141 Abn86141 Rice dise
c	544	3	30.0	23	6	ABN86141 Abn86141 Rice dise
	545	3	30.0	23	8	ABZ68829 Abz68829 Primer us
c	546	3	30.0	23	8	ABZ68829 Abz68829 Primer us
	547	3	30.0	23	10	ADF55283 Adf55283 SINE fami
c	548	3	30.0	23	10	ADF55283 Adf55283 SINE fami
	549	3	30.0	23	12	ADK67521 Adk67521 Lactobaci
c	550	3	30.0	23	12	ADK67521 Adk67521 Lactobaci
	551	3	30.0	23	12	ADN96905 Adn96905 Immunosti
c	552	3	30.0	23	12	ADN96905 Adn96905 Immunosti
	553	3	30.0	23	12	ADN96970 Adn96970 Immunosti
c	554	3	30.0	23	12	ADN96970 Adn96970 Immunosti
	555	3	30.0	23	12	ADN96925 Adn96925 Immunosti
c	556	3	30.0	23	12	ADN96925 Adn96925 Immunosti
	557	3	30.0	23	12	ADN96945 Adn96945 Immunosti
c	558	3	30.0	23	12	ADN96945 Adn96945 Immunosti
	559	3	30.0	23	12	ADN97000 Adn97000 Immunosti
c	560	3	30.0	23	12	ADN97000 Adn97000 Immunosti
	561	3	30.0	23	12	ADN96895 Adn96895 Immunosti
c	562	3	30.0	23	12	ADN96895 Adn96895 Immunosti
	563	3	30.0	23	12	ADN96915 Adn96915 Immunosti
c	564	3	30.0	23	12	ADN96915 Adn96915 Immunosti
	565	3	30.0	23	12	ADN96935 Adn96935 Immunosti
c	566	3	30.0	23	12	ADN96935 Adn96935 Immunosti
	567	3	30.0	23	12	ADN96990 Adn96990 Immunosti
c	568	3	30.0	23	12	ADN96990 Adn96990 Immunosti
	569	3	30.0	23	12	ADN96980 Adn96980 Immunosti
c	570	3	30.0	23	12	ADN96980 Adn96980 Immunosti
	571	3	30.0	24	2	AAQ25605 Aaq25605 Enterotox
c	572	3	30.0	24	2	AAQ25605 Aaq25605 Enterotox
	573	3	30.0	24	2	AAQ25606 Aaq25606 Enterotox
c	574	3	30.0	24	2	AAQ25606 Aaq25606 Enterotox
	575	3	30.0	24	2	AAT18361 Aat18361 G-protein
c	576	3	30.0	24	2	AAT18361 Aat18361 G-protein
	577	3	30.0	24	2	AAT34157 Aat34157 Monoclona
c	578	3	30.0	24	2	AAT34157 Aat34157 Monoclona
	579	3	30.0	24	2	AAX86619 Aax86619 Probe for
c	580	3	30.0	24	2	AAX86619 Aax86619 Probe for
	581	3	30.0	24	3	AAA38622 Aaa38622 Degenerat
c	582	3	30.0	24	3	AAA38622 Aaa38622 Degenerat
	583	3	30.0	24	3	AAA56655 Aaa56655 Murine ka
c	584	3	30.0	24	3	AAA56655 Aaa56655 Murine ka
	585	3	30.0	24	3	AAA56657 Aaa56657 Murine ka
c	586	3	30.0	24	3	AAA56657 Aaa56657 Murine ka
	587	3	30.0	24	4	AAS13046 Aas13046 Primer #2
c	588	3	30.0	24	4	AAS13046 Aas13046 Primer #2
	589	3	30.0	24	8	ACC41596 Acc41596 Human zin
c	590	3	30.0	24	8	ACC41596 Acc41596 Human zin
	591	3	30.0	24	10	ADC36583 Adc36583 Primer of
c	592	3	30.0	24	10	ADC36583 Adc36583 Primer of
	593	3	30.0	24	10	AAD60266 Aad60266 Human SNO
c	594	3	30.0	24	10	AAD60266 Aad60266 Human SNO
	595	3	30.0	24	12	ADN96906 Adn96906 Immunosti
c	596	3	30.0	24	12	ADN96906 Adn96906 Immunosti
	597	3	30.0	24	12	ADN97011 Adn97011 Immunosti
c	598	3	30.0	24	12	ADN97011 Adn97011 Immunosti
	599	3	30.0	24	12	ADN96896 Adn96896 Immunosti
c	600	3	30.0	24	12	ADN96896 Adn96896 Immunosti
	601	3	30.0	24	12	ADN96981 Adn96981 Immunosti
c	602	3	30.0	24	12	ADN96981 Adn96981 Immunosti
	603	3	30.0	24	12	ADN96956 Adn96956 Immunosti
c	604	3	30.0	24	12	ADN96956 Adn96956 Immunosti
	605	3	30.0	24	12	ADN97001 Adn97001 Immunosti
c	606	3	30.0	24	12	ADN97001 Adn97001 Immunosti
	607	3	30.0	24	12	ADN96936 Adn96936 Immunosti
c	608	3	30.0	24	12	ADN96936 Adn96936 Immunosti
	609	3	30.0	24	12	ADN96926 Adn96926 Immunosti
c	610	3	30.0	24	12	ADN96926 Adn96926 Immunosti
	611	3	30.0	24	12	ADN96916 Adn96916 Immunosti
c	612	3	30.0	24	12	ADN96916 Adn96916 Immunosti
	613	3	30.0	24	12	ADN96946 Adn96946 Immunosti
c	614	3	30.0	24	12	ADN96946 Adn96946 Immunosti
	615	3	30.0	24	12	ADN96971 Adn96971 Immunosti
c	616	3	30.0	24	12	ADN96971 Adn96971 Immunosti
	617	3	30.0	24	12	ADN96991 Adn96991 Immunosti
c	618	3	30.0	24	12	ADN96991 Adn96991 Immunosti
	619	3	30.0	25	2	AAQ24777 Aaq24777 Arbitrary
c	620	3	30.0	25	2	AAQ24777 Aaq24777 Arbitrary
	621	3	30.0	25	2	AAT16363 Aat16363 AP-PCR Kp
c	622	3	30.0	25	2	AAT16363 Aat16363 AP-PCR Kp
	623	3	30.0	25	2	AAV81475 Aav81475 SacI prim
c	624	3	30.0	25	2	AAV81475 Aav81475 SacI prim
	625	3	30.0	25	3	AAZ91750 Aaz91750 PCR prime
c	626	3	30.0	25	3	AAZ91750 Aaz91750 PCR prime
	627	3	30.0	25	6	ABS54567 Abs54567 12088sXXY
c	628	3	30.0	25	6	ABS54567 Abs54567 12088sXXY
	629	3	30.0	25	6	ABS54566 Abs54566 12088sXXY
c	630	3	30.0	25	6	ABS54566 Abs54566 12088sXXY
	631	3	30.0	25	6	ABL61010 Abl61010 B. mori T
c	632	3	30.0	25	6	ABL61010 Abl61010 B. mori T
	633	3	30.0	25	8	AAL41326 Aal41326 Promoter
c	634	3	30.0	25	8	AAL41326 Aal41326 Promoter
	635	3	30.0	25	8	ABZ68817 Abz68817 Nucleotid
c	636	3	30.0	25	8	ABZ68817 Abz68817 Nucleotid
	637	3	30.0	25	12	ADJ63789 Adj63789 Primer #1
c	638	3	30.0	25	12	ADJ63789 Adj63789 Primer #1
	639	3	30.0	25	12	ADN97012 Adn97012 Immunosti
c	640	3	30.0	25	12	ADN97012 Adn97012 Immunosti
	641	3	30.0	25	12	ADN96927 Adn96927 Immunosti
c	642	3	30.0	25	12	ADN96927 Adn96927 Immunosti
	643	3	30.0	25	12	ADN96972 Adn96972 Immunosti
c	644	3	30.0	25	12	ADN96972 Adn96972 Immunosti
	645	3	30.0	25	12	ADN96982 Adn96982 Immunosti
c	646	3	30.0	25	12	ADN96982 Adn96982 Immunosti
	647	3	30.0	25	12	ADN96907 Adn96907 Immunosti
c	648	3	30.0	25	12	ADN96907 Adn96907 Immunosti
	649	3	30.0	25	12	ADN97002 Adn97002 Immunosti
c	650	3	30.0	25	12	ADN97002 Adn97002 Immunosti
	651	3	30.0	25	12	ADN96917 Adn96917 Immunosti
c	652	3	30.0	25	12	ADN96917 Adn96917 Immunosti
	653	3	30.0	25	12	ADN96897 Adn96897 Immunosti
c	654	3	30.0	25	12	ADN96897 Adn96897 Immunosti
	655	3	30.0	25	12	ADN96992 Adn96992 Immunosti
c	656	3	30.0	25	12	ADN96992 Adn96992 Immunosti
	657	3	30.0	25	12	ADN97022 Adn97022 Immunosti
c	658	3	30.0	25	12	ADN97022 Adn97022 Immunosti
	659	3	30.0	25	12	ADN96947 Adn96947 Immunosti
c	660	3	30.0	25	12	ADN96947 Adn96947 Immunosti
	661	3	30.0	25	12	ADN96957 Adn96957 Immunosti
c	662	3	30.0	25	12	ADN96957 Adn96957 Immunosti
	663	3	30.0	25	12	ADN96937 Adn96937 Immunosti
c	664	3	30.0	25	12	ADN96937 Adn96937 Immunosti
	665	3	30.0	25	12	ADP81364 Adp81364 Vibrio sp
c	666	3	30.0	25	12	ADP81364 Adp81364 Vibrio sp
	667	3	30.0	26	2	AAQ29967 Aaq29967 PCR prime
c	668	3	30.0	26	2	AAQ29967 Aaq29967 PCR prime
	669	3	30.0	26	2	AAQ91417 Aaq91417 Human olf
c	670	3	30.0	26	2	AAQ91417 Aaq91417 Human olf
	671	3	30.0	26	2	AAT07997 Aat07997 HIV-1 rev
c	672	3	30.0	26	2	AAT07997 Aat07997 HIV-1 rev
	673	3	30.0	26	2	AAT11320 Aat11320 Helicobac
c	674	3	30.0	26	2	AAT11320 Aat11320 Helicobac
	675	3	30.0	26	2	AAT10875 Aat10875 H. pylori
c	676	3	30.0	26	2	AAT10875 Aat10875 H. pylori
	677	3	30.0	26	2	AAT16365 Aat16365 AP-PCR Kp
c	678	3	30.0	26	2	AAT16365 Aat16365 AP-PCR Kp

679	3	30.0	26	2	AAT51555	Aat51555	Herpes vi
c 680	3	30.0	26	2	AAT51555	Aat51555	Herpes vi
681	3	30.0	26	2	AAT51556	Aat51556	Herpes vi
c 682	3	30.0	26	2	AAT51556	Aat51556	Herpes vi
683	3	30.0	26	2	AAT65454	Aat65454	Human ker
c 684	3	30.0	26	2	AAT65454	Aat65454	Human ker
685	3	30.0	26	2	AAV14871	Aav14871	SELEX ide
c 686	3	30.0	26	2	AAV14871	Aav14871	SELEX ide
687	3	30.0	26	2	AAV79943	Aav79943	Sequence
c 688	3	30.0	26	2	AAV79943	Aav79943	Sequence
689	3	30.0	26	2	AAX25798	Aax25798	Probe tar
c 690	3	30.0	26	2	AAX25798	Aax25798	Probe tar
691	3	30.0	26	3	AAA93043	Aaa93043	High-affi
c 692	3	30.0	26	3	AAA93043	Aaa93043	High-affi
693	3	30.0	26	4	AAS04155	Aas04155	Primer Kp
c 694	3	30.0	26	4	AAS04155	Aas04155	Primer Kp
695	3	30.0	26	4	AAH00643	Aah00643	Candida d
c 696	3	30.0	26	4	AAH00643	Aah00643	Candida d
697	3	30.0	26	6	ABK61419	Abk61419	SELEX pro
c 698	3	30.0	26	6	ABK61419	Abk61419	SELEX pro
699	3	30.0	26	6	ABL76870	Abl76870	Bacterial
c 700	3	30.0	26	6	ABL76870	Abl76870	Bacterial
701	3	30.0	26	6	ABK67434	Abk67434	Calcium t
c 702	3	30.0	26	6	ABK67434	Abk67434	Calcium t
703	3	30.0	26	6	ABK67433	Abk67433	Calcium t
c 704	3	30.0	26	6	ABK67433	Abk67433	Calcium t
705	3	30.0	26	10	ADC16267	Adc16267	Chlamydia
c 706	3	30.0	26	10	ADC16267	Adc16267	Chlamydia
707	3	30.0	26	10	ADF67807	Adf67807	SELEX-rel
c 708	3	30.0	26	10	ADF67807	Adf67807	SELEX-rel
709	3	30.0	26	12	ADG39355	Adg39355	SELEX ass
c 710	3	30.0	26	12	ADG39355	Adg39355	SELEX ass
711	3	30.0	26	12	ADJ63792	Adj63792	Kpn-R rel
c 712	3	30.0	26	12	ADJ63792	Adj63792	Kpn-R rel
713	3	30.0	26	12	ADN96898	Adn96898	Immunosti
c 714	3	30.0	26	12	ADN96898	Adn96898	Immunosti
715	3	30.0	26	12	ADN96928	Adn96928	Immunosti
c 716	3	30.0	26	12	ADN96928	Adn96928	Immunosti
717	3	30.0	26	12	ADN97003	Adn97003	Immunosti
c 718	3	30.0	26	12	ADN97003	Adn97003	Immunosti
719	3	30.0	26	12	ADN96958	Adn96958	Immunosti
c 720	3	30.0	26	12	ADN96958	Adn96958	Immunosti
721	3	30.0	26	12	ADN96983	Adn96983	Immunosti
c 722	3	30.0	26	12	ADN96983	Adn96983	Immunosti
723	3	30.0	26	12	ADN97033	Adn97033	Immunosti
c 724	3	30.0	26	12	ADN97033	Adn97033	Immunosti
725	3	30.0	26	12	ADN96918	Adn96918	Immunosti
c 726	3	30.0	26	12	ADN96918	Adn96918	Immunosti
727	3	30.0	26	12	ADN96948	Adn96948	Immunosti
c 728	3	30.0	26	12	ADN96948	Adn96948	Immunosti
729	3	30.0	26	12	ADN96973	Adn96973	Immunosti
c 730	3	30.0	26	12	ADN96973	Adn96973	Immunosti
731	3	30.0	26	12	ADN96908	Adn96908	Immunosti
c 732	3	30.0	26	12	ADN96908	Adn96908	Immunosti
733	3	30.0	26	12	ADN97013	Adn97013	Immunosti
c 734	3	30.0	26	12	ADN97013	Adn97013	Immunosti
735	3	30.0	26	12	ADN96938	Adn96938	Immunosti
c 736	3	30.0	26	12	ADN96938	Adn96938	Immunosti
737	3	30.0	26	12	ADN97023	Adn97023	Immunosti
c 738	3	30.0	26	12	ADN97023	Adn97023	Immunosti
739	3	30.0	26	12	ADN96993	Adn96993	Immunosti
c 740	3	30.0	26	12	ADN96993	Adn96993	Immunosti
741	3	30.0	27	2	AAT07654	Aat07654	Ligand fo
c 742	3	30.0	27	2	AAT07654	Aat07654	Ligand fo
743	3	30.0	27	2	AAT62502	Aat62502	Murine re
c 744	3	30.0	27	2	AAT62502	Aat62502	Murine re
745	3	30.0	27	2	AAT65453	Aat65453	Human ker
c 746	3	30.0	27	2	AAT65453	Aat65453	Human ker
747	3	30.0	27	2	AAT92809	Aat92809	Primer KV
c 748	3	30.0	27	2	AAT92809	Aat92809	Primer KV
749	3	30.0	27	2	AAV26559	Aav26559	Human IP-
c 750	3	30.0	27	2	AAV26559	Aav26559	Human IP-
751	3	30.0	27	2	AAV52806	Aav52806	Immunoglo
c 752	3	30.0	27	2	AAV52806	Aav52806	Immunoglo
753	3	30.0	27	2	AAV14865	Aav14865	SELEX ide
c 754	3	30.0	27	2	AAV14865	Aav14865	SELEX ide
755	3	30.0	27	2	AAZ23273	Aaz23273	Mouse str
c 756	3	30.0	27	2	AAZ23273	Aaz23273	Mouse str
757	3	30.0	27	2	AAV79937	Aav79937	Sequence
c 758	3	30.0	27	2	AAV79937	Aav79937	Sequence
759	3	30.0	27	3	AAZ40328	Aaz40328	PCR prime
c 760	3	30.0	27	3	AAZ40328	Aaz40328	PCR prime
761	3	30.0	27	3	AAZ40329	Aaz40329	PCR prime
c 762	3	30.0	27	3	AAZ40329	Aaz40329	PCR prime
763	3	30.0	27	3	AAZ99852	Aaz99852	PCR prime
c 764	3	30.0	27	3	AAZ99852	Aaz99852	PCR prime
765	3	30.0	27	3	AAZ99865	Aaz99865	Degenerat
c 766	3	30.0	27	3	AAZ99865	Aaz99865	Degenerat
767	3	30.0	27	3	AAS14490	Aas14490	Primer #1
c 768	3	30.0	27	3	AAS14490	Aas14490	Primer #1
769	3	30.0	27	3	AAA09969	Aaa09969	Primer KV
c 770	3	30.0	27	3	AAA09969	Aaa09969	Primer KV
771	3	30.0	27	3	AAA93037	Aaa93037	High-affi
c 772	3	30.0	27	3	AAA93037	Aaa93037	High-affi
773	3	30.0	27	4	AAS04150	Aas04150	Degenerat
c 774	3	30.0	27	4	AAS04150	Aas04150	Degenerat
775	3	30.0	27	4	AAF25739	Aaf25739	Tobacco i
c 776	3	30.0	27	4	AAF25739	Aaf25739	Tobacco i
777	3	30.0	27	6	ABK61413	Abk61413	SELEX pro
c 778	3	30.0	27	6	ABK61413	Abk61413	SELEX pro
779	3	30.0	27	6	ABV74339	Abv74339	Ribozyme
c 780	3	30.0	27	6	ABV74339	Abv74339	Ribozyme
781	3	30.0	27	8	ACC47722	Acc47722	A. niger
c 782	3	30.0	27	8	ACC47722	Acc47722	A. niger
783	3	30.0	27	9	ACD13457	Acd13457	Degenerat
c 784	3	30.0	27	9	ACD13457	Acd13457	Degenerat
785	3	30.0	27	9	ACD13458	Acd13458	Degenerat
c 786	3	30.0	27	9	ACD13458	Acd13458	Degenerat
787	3	30.0	27	10	AAD60860	Aad60860	Primer #1
c 788	3	30.0	27	10	AAD60860	Aad60860	Primer #1
789	3	30.0	27	10	AAD60859	Aad60859	Primer #9
c 790	3	30.0	27	10	AAD60859	Aad60859	Primer #9
791	3	30.0	27	10	ADF67801	Adf67801	SELEX-rel
c 792	3	30.0	27	10	ADF67801	Adf67801	SELEX-rel
793	3	30.0	27	10	ADJ72471	Adj72471	Human GP1
c 794	3	30.0	27	10	ADJ72471	Adj72471	Human GP1
795	3	30.0	27	10	ADJ72472	Adj72472	Human GP1
c 796	3	30.0	27	10	ADJ72472	Adj72472	Human GP1
797	3	30.0	27	11	ADM11586	Adm11586	Amplifica
c 798	3	30.0	27	11	ADM11586	Adm11586	Amplifica
799	3	30.0	27	12	ADG39349	Adg39349	SELEX ass
c 800	3	30.0	27	12	ADG39349	Adg39349	SELEX ass
801	3	30.0	27	12	ADI36428	Adi36428	Human VH
c 802	3	30.0	27	12	ADI36428	Adi36428	Human VH
803	3	30.0	27	12	ADN96984	Adn96984	Immunosti
c 804	3	30.0	27	12	ADN96984	Adn96984	Immunosti
805	3	30.0	27	12	ADN96929	Adn96929	Immunosti
c 806	3	30.0	27	12	ADN96929	Adn96929	Immunosti
807	3	30.0	27	12	ADN96919	Adn96919	Immunosti
c 808	3	30.0	27	12	ADN96919	Adn96919	Immunosti
809	3	30.0	27	12	ADN97024	Adn97024	Immunosti
c 810	3	30.0	27	12	ADN97024	Adn97024	Immunosti
811	3	30.0	27	12	ADN97014	Adn97014	Immunosti
c 812	3	30.0	27	12	ADN97014	Adn97014	Immunosti
813	3	30.0	27	12	ADN96909	Adn96909	Immunosti
c 814	3	30.0	27	12	ADN96909	Adn96909	Immunosti
815	3	30.0	27	12	ADN96959	Adn96959	Immunosti
c 816	3	30.0	27	12	ADN96959	Adn96959	Immunosti
817	3	30.0	27	12	ADN97004	Adn97004	Immunosti
c 818	3	30.0	27	12	ADN97004	Adn97004	Immunosti
819	3	30.0	27	12	ADN96939	Adn96939	Immunosti
c 820	3	30.0	27	12	ADN96939	Adn96939	Immunosti
821	3	30.0	27	12	ADN97034	Adn97034	Immunosti
c 822	3	30.0	27	12	ADN97034	Adn97034	Immunosti
823	3	30.0	27	12	ADN96974	Adn96974	Immunosti
c 824	3	30.0	27	12	ADN96974	Adn96974	Immunosti

	825	3	30.0	27	12	ADN96949 Adn96949 Immunosti
c	826	3	30.0	27	12	ADN96949 Adn96949 Immunosti
	827	3	30.0	27	12	ADN96994 Adn96994 Immunosti
c	828	3	30.0	27	12	ADN96994 Adn96994 Immunosti
	829	3	30.0	28	2	AAQ68804 Aaq68804 Degenerat
c	830	3	30.0	28	2	AAQ68804 Aaq68804 Degenerat
	831	3	30.0	28	2	AAV26773 Aav26773 Anti-gp54
c	832	3	30.0	28	2	AAV26773 Aav26773 Anti-gp54
	833	3	30.0	28	2	AAX24388 Aax24388 Chemokine
c	834	3	30.0	28	2	AAX24388 Aax24388 Chemokine
	835	3	30.0	28	6	AAD22469 Aad22469 Rhesus ma
c	836	3	30.0	28	6	AAD22469 Aad22469 Rhesus ma
	837	3	30.0	28	6	AAD39252 Aad39252 Non-human
c	838	3	30.0	28	6	AAD39252 Aad39252 Non-human
	839	3	30.0	28	10	ACF04748 Acf04748 Degenerat
c	840	3	30.0	28	10	ACF04748 Acf04748 Degenerat
	841	3	30.0	28	12	ADN96920 Adn96920 Immunosti
c	842	3	30.0	28	12	ADN96920 Adn96920 Immunosti
	843	3	30.0	28	12	ADN96975 Adn96975 Immunosti
c	844	3	30.0	28	12	ADN96975 Adn96975 Immunosti
	845	3	30.0	28	12	ADN96960 Adn96960 Immunosti
c	846	3	30.0	28	12	ADN96960 Adn96960 Immunosti
	847	3	30.0	28	12	ADN96930 Adn96930 Immunosti
c	848	3	30.0	28	12	ADN96930 Adn96930 Immunosti
	849	3	30.0	28	12	ADN97025 Adn97025 Immunosti
c	850	3	30.0	28	12	ADN97025 Adn97025 Immunosti
	851	3	30.0	28	12	ADN96995 Adn96995 Immunosti
c	852	3	30.0	28	12	ADN96995 Adn96995 Immunosti
	853	3	30.0	28	12	ADN97005 Adn97005 Immunosti
c	854	3	30.0	28	12	ADN97005 Adn97005 Immunosti
	855	3	30.0	28	12	ADN96940 Adn96940 Immunosti
c	856	3	30.0	28	12	ADN96940 Adn96940 Immunosti
	857	3	30.0	28	12	ADN96950 Adn96950 Immunosti
c	858	3	30.0	28	12	ADN96950 Adn96950 Immunosti
	859	3	30.0	28	12	ADN97015 Adn97015 Immunosti
c	860	3	30.0	28	12	ADN97015 Adn97015 Immunosti
	861	3	30.0	28	12	ADN97035 Adn97035 Immunosti
c	862	3	30.0	28	12	ADN97035 Adn97035 Immunosti
	863	3	30.0	28	12	ADN96985 Adn96985 Immunosti
c	864	3	30.0	28	12	ADN96985 Adn96985 Immunosti
	865	3	30.0	29	2	AAQ20235 Aaq20235 T-cell re
c	866	3	30.0	29	2	AAQ20235 Aaq20235 T-cell re
	867	3	30.0	29	2	AAQ71595 Aaq71595 Mycobacte
c	868	3	30.0	29	2	AAQ71595 Aaq71595 Mycobacte
	869	3	30.0	29	2	AAT07996 Aat07996 HIV-1 rev
c	870	3	30.0	29	2	AAT07996 Aat07996 HIV-1 rev
	871	3	30.0	29	2	AAT16128 Aat16128 Mycobacte
c	872	3	30.0	29	2	AAT16128 Aat16128 Mycobacte
	873	3	30.0	29	2	AAV54321 Aav54321 T-cell re
c	874	3	30.0	29	2	AAV54321 Aav54321 T-cell re
	875	3	30.0	29	2	AAV14870 Aav14870 SELEX ide
c	876	3	30.0	29	2	AAV14870 Aav14870 SELEX ide
	877	3	30.0	29	2	AAV79942 Aav79942 Sequence
c	878	3	30.0	29	2	AAV79942 Aav79942 Sequence
	879	3	30.0	29	2	AAX55404 Aax55404 Primer to
c	880	3	30.0	29	2	AAX55404 Aax55404 Primer to
	881	3	30.0	29	3	AAA93042 Aaa93042 High-affi
c	882	3	30.0	29	3	AAA93042 Aaa93042 High-affi
	883	3	30.0	29	6	ABK61418 Abk61418 SELEX pro
c	884	3	30.0	29	6	ABK61418 Abk61418 SELEX pro
	885	3	30.0	29	6	ABV74340 Abv74340 Ribozyme
c	886	3	30.0	29	6	ABV74340 Abv74340 Ribozyme
	887	3	30.0	29	9	ACF04147 Acf04147 Factor V
c	888	3	30.0	29	9	ACF04147 Acf04147 Factor V
	889	3	30.0	29	9	ACF04149 Acf04149 Factor V
c	890	3	30.0	29	9	ACF04149 Acf04149 Factor V
	891	3	30.0	29	10	ADF67806 Adf67806 SELEX-rel
c	892	3	30.0	29	10	ADF67806 Adf67806 SELEX-rel
	893	3	30.0	29	12	ADG39354 Adg39354 SELEX ass
c	894	3	30.0	29	12	ADG39354 Adg39354 SELEX ass
	895	3	30.0	29	12	ADM97972 Adm97972 Sesquiter
c	896	3	30.0	29	12	ADM97972 Adm97972 Sesquiter
	897	3	30.0	29	12	ADN96931 Adn96931 Immunosti
c	898	3	30.0	29	12	ADN96931 Adn96931 Immunosti
	899	3	30.0	29	12	ADN97016 Adn97016 Immunosti
c	900	3	30.0	29	12	ADN97016 Adn97016 Immunosti
	901	3	30.0	29	12	ADN97036 Adn97036 Immunosti
c	902	3	30.0	29	12	ADN97036 Adn97036 Immunosti
	903	3	30.0	29	12	ADN96986 Adn96986 Immunosti
c	904	3	30.0	29	12	ADN96986 Adn96986 Immunosti
	905	3	30.0	29	12	ADN97026 Adn97026 Immunosti
c	906	3	30.0	29	12	ADN97026 Adn97026 Immunosti
	907	3	30.0	29	12	ADN96941 Adn96941 Immunosti
c	908	3	30.0	29	12	ADN96941 Adn96941 Immunosti
	909	3	30.0	29	12	ADN97006 Adn97006 Immunosti
c	910	3	30.0	29	12	ADN97006 Adn97006 Immunosti
	911	3	30.0	29	12	ADN96961 Adn96961 Immunosti
c	912	3	30.0	29	12	ADN96961 Adn96961 Immunosti
	913	3	30.0	29	12	ADN96996 Adn96996 Immunosti
c	914	3	30.0	29	12	ADN96996 Adn96996 Immunosti
	915	3	30.0	29	12	ADN96951 Adn96951 Immunosti
c	916	3	30.0	29	12	ADN96951 Adn96951 Immunosti
	917	3	30.0	30	2	AAQ45812 Aaq45812 HBV ampli
c	918	3	30.0	30	2	AAQ45812 Aaq45812 HBV ampli
	919	3	30.0	30	2	AAV07809 Aav07809 HBV.D47 a
c	920	3	30.0	30	2	AAV07809 Aav07809 HBV.D47 a
	921	3	30.0	30	2	AAV83038 Aav83038 Amplifier
c	922	3	30.0	30	2	AAV83038 Aav83038 Amplifier
	923	3	30.0	30	5	AAS00637 Aas00637 DNA encod
c	924	3	30.0	30	5	AAS00637 Aas00637 DNA encod
	925	3	30.0	30	6	ABA99401 Aba99401 B. mori T
c	926	3	30.0	30	6	ABA99401 Aba99401 B. mori T
	927	3	30.0	30	10	ADF44295 Adf44295 HPV PCR p
c	928	3	30.0	30	10	ADF44295 Adf44295 HPV PCR p
	929	3	30.0	30	10	ADF29179 Adf29179 Binding o
c	930	3	30.0	30	10	ADF29179 Adf29179 Binding o
	931	3	30.0	30	12	ADN96952 Adn96952 Immunosti
c	932	3	30.0	30	12	ADN96952 Adn96952 Immunosti
	933	3	30.0	30	12	ADN96942 Adn96942 Immunosti
c	934	3	30.0	30	12	ADN96942 Adn96942 Immunosti
	935	3	30.0	30	12	ADN97027 Adn97027 Immunosti
c	936	3	30.0	30	12	ADN97027 Adn97027 Immunosti
	937	3	30.0	30	12	ADN96962 Adn96962 Immunosti
c	938	3	30.0	30	12	ADN96962 Adn96962 Immunosti
	939	3	30.0	30	12	ADN97017 Adn97017 Immunosti
c	940	3	30.0	30	12	ADN97017 Adn97017 Immunosti
	941	3	30.0	30	12	ADN97037 Adn97037 Immunosti
c	942	3	30.0	30	12	ADN97037 Adn97037 Immunosti
	943	3	30.0	30	12	ADN97007 Adn97007 Immunosti
c	944	3	30.0	30	12	ADN97007 Adn97007 Immunosti
	945	3	30.0	30	12	ADN96997 Adn96997 Immunosti
c	946	3	30.0	30	12	ADN96997 Adn96997 Immunosti
	947	3	30.0	31	2	AAQ91556 Aaq91556 Esterase
c	948	3	30.0	31	2	AAQ91556 Aaq91556 Esterase
	949	3	30.0	31	2	AAQ83905 Aaq83905 Hepatitis
c	950	3	30.0	31	2	AAQ83905 Aaq83905 Hepatitis
	951	3	30.0	31	2	AAT16665 Aat16665 Hepatitis
c	952	3	30.0	31	2	AAT16665 Aat16665 Hepatitis
	953	3	30.0	31	2	AAT36502 Aat36502 Primer DN
c	954	3	30.0	31	2	AAT36502 Aat36502 Primer DN
	955	3	30.0	31	6	AAD29661 Aad29661 Human cat
c	956	3	30.0	31	6	AAD29661 Aad29661 Human cat
	957	3	30.0	31	10	ADC77494 Adc77494 Hyalurona
c	958	3	30.0	31	10	ADC77494 Adc77494 Hyalurona
	959	3	30.0	31	10	ADF29177 Adf29177 Binding o
c	960	3	30.0	31	10	ADF29177 Adf29177 Binding o
	961	3	30.0	31	12	ADN96953 Adn96953 Immunosti
c	962	3	30.0	31	12	ADN96953 Adn96953 Immunosti
	963	3	30.0	31	12	ADN97038 Adn97038 Immunosti
c	964	3	30.0	31	12	ADN97038 Adn97038 Immunosti
	965	3	30.0	31	12	ADN96963 Adn96963 Immunosti
c	966	3	30.0	31	12	ADN96963 Adn96963 Immunosti
	967	3	30.0	31	12	ADN97008 Adn97008 Immunosti
c	968	3	30.0	31	12	ADN97008 Adn97008 Immunosti
	969	3	30.0	31	12	ADN97018 Adn97018 Immunosti
c	970	3	30.0	31	12	ADN97018 Adn97018 Immunosti

971	3	30.0	31	12	ADN97028	Adn97028 Immunosti
c 972	3	30.0	31	12	ADN97028	Adn97028 Immunosti
973	3	30.0	32	2	AAQ06407	Aaq06407 Probe for
c 974	3	30.0	32	2	AAQ06407	Aaq06407 Probe for
975	3	30.0	32	2	AAX58849	Aax58849 Hyalurona
c 976	3	30.0	32	2	AAX58849	Aax58849 Hyalurona
977	3	30.0	32	2	AAX21259	Aax21259 Primer PR
c 978	3	30.0	32	2	AAX21259	Aax21259 Primer PR
979	3	30.0	32	3	AAA98231	Aaa98231 Human ret
c 980	3	30.0	32	3	AAA98231	Aaa98231 Human ret
981	3	30.0	32	8	ABQ77386	Abq77386 Parsley F
c 982	3	30.0	32	8	ABQ77386	Abq77386 Parsley F
983	3	30.0	32	8	ABV74015	Abv74015 Isoflavon
c 984	3	30.0	32	8	ABV74015	Abv74015 Isoflavon
985	3	30.0	32	10	ADF61701	Adf61701 Prion bin
c 986	3	30.0	32	10	ADF61701	Adf61701 Prion bin
987	3	30.0	32	12	ADN97019	Adn97019 Immunosti
c 988	3	30.0	32	12	ADN97019	Adn97019 Immunosti
989	3	30.0	32	12	ADN96964	Adn96964 Immunosti
c 990	3	30.0	32	12	ADN96964	Adn96964 Immunosti
991	3	30.0	32	12	ADN97039	Adn97039 Immunosti
c 992	3	30.0	32	12	ADN97039	Adn97039 Immunosti
993	3	30.0	32	12	ADN97029	Adn97029 Immunosti
c 994	3	30.0	32	12	ADN97029	Adn97029 Immunosti
995	3	30.0	33	2	AAQ31144	Aaq31144 Probe 113
c 996	3	30.0	33	2	AAQ31144	Aaq31144 Probe 113
997	3	30.0	33	2	AAQ31131	Aaq31131 Probe 100
c 998	3	30.0	33	2	AAQ31131	Aaq31131 Probe 100
999	3	30.0	33	2	AAQ31134	Aaq31134 Probe 103
c1000	3	30.0	33	2	AAQ31134	Aaq31134 Probe 103

ALIGNMENTS

```
RESULT 1
AAQ31948
ID   AAQ31948 standard; DNA; 10 BP.
XX
AC   AAQ31948;
XX
DT   25-MAR-2003  (revised)
DT   27-APR-1993  (first entry)
XX
DE   Monomeric p53-specific DNA binding site.
XX
KW   P53; DNA-binding; cancer; neoplasia; tumour; ds.
XX
OS   Synthetic.
XX
PN   EP518650-A2.
XX
PD   16-DEC-1992.
XX
PF   10-JUN-1992;   92EP-00305333.
XX
PR   14-JUN-1991;   91US-00715182.
PR   31-MAR-1992;   92US-00860758.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
PA   (PHAR-) PHARMAGENICS INC.
XX
PI   Vogelstein B,  Kinzler KW,  Sherman MI;
XX
DR   WPI; 1992-417505/51.
XX
PT   Detection and expression of wild type P53 protein - useful for diagnosing
PT   and treating cancers, and for screening potential chemotherapeutic
PT   agents.
XX
PS   Claim 22; Page 24; 51pp; English.
XX
CC   Wild-type p53 protein binds specific fragments of human chromosomal DNA.
CC   Each fragment contains no more than one monomer of the double stranded
CC   sequence shown separated by 0-13 base pairs. Some of these sequences are
CC   found near the origin of replication of certain animal viruses and animal
CC   cells. Four mutant forms of p53 protein which are commonly found in human
CC   tumours do not have the ability to bind to these sequences. Thus a
CC   function of p53 may be mediated by its ability to bind specific DNA
CC   sequences in the human genome. The sequence shown is a consensus sequence
CC   for p53 DNA binding. When inserted upstream and adjacent to a reporter
CC   gene the sequence allows identification of wild type p53, and such a
CC   construct could be used for diagnosis of p53 mutations and onset and
CC   development of various cancers. The construct may also be used to screen
CC   potential chemotherapeutic agents and to identify agents which
CC   specifically bind p53-specific DNA. Also wild-type p53 gene function may
CC   be restored to neoplastic cells having a mutation in their p53 gene. See
CC   also AAQ31949-84. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 2
AAQ31948/c
ID   AAQ31948 standard; DNA; 10 BP.
XX
AC   AAQ31948;
XX
DT   25-MAR-2003  (revised)
DT   27-APR-1993  (first entry)
XX
DE   Monomeric p53-specific DNA binding site.
XX
KW   P53; DNA-binding; cancer; neoplasia; tumour; ds.
XX
OS   Synthetic.
XX
PN   EP518650-A2.
XX
PD   16-DEC-1992.
XX
PF   10-JUN-1992;   92EP-00305333.
XX
PR   14-JUN-1991;   91US-00715182.
PR   31-MAR-1992;   92US-00860758.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
PA   (PHAR-) PHARMAGENICS INC.
XX
PI   Vogelstein B,  Kinzler KW,  Sherman MI;
XX
DR   WPI; 1992-417505/51.
XX
PT   Detection and expression of wild type P53 protein - useful for diagnosing
PT   and treating cancers, and for screening potential chemotherapeutic
PT   agents.
XX
PS   Claim 22; Page 24; 51pp; English.
XX
CC   Wild-type p53 protein binds specific fragments of human chromosomal DNA.
CC   Each fragment contains no more than one monomer of the double stranded
CC   sequence shown separated by 0-13 base pairs. Some of these sequences are
CC   found near the origin of replication of certain animal viruses and animal
CC   cells. Four mutant forms of p53 protein which are commonly found in human
CC   tumours do not have the ability to bind to these sequences. Thus a
CC   function of p53 may be mediated by its ability to bind specific DNA
CC   sequences in the human genome. The sequence shown is a consensus sequence
CC   for p53 DNA binding. When inserted upstream and adjacent to a reporter
```

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CC   gene the sequence allows identification of wild type p53, and such a
CC   construct could be used for diagnosis of p53 mutations and onset and
CC   development of various cancers. The construct may also be used to screen
CC   potential chemotherapeutic agents and to identify agents which
CC   specifically bind p53-specific DNA. Also wild-type p53 gene function may
CC   be restored to neoplastic cells having a mutation in their p53 gene. See
CC   also AAQ31949-84. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 3
AAV45242
ID   AAV45242 standard; DNA; 10 BP.
XX
AC   AAV45242;
XX
DT   09-NOV-1998  (first entry)
XX
DE   Human nerve growth factor exon promoter consensus binding motif.
XX
KW   NGF; nerve growth factor; treatment; promoter; neurodegenerative disease;
KW   consensus binding motif; ds.
XX
OS   Homo sapiens.
XX
PN   WO9835027-A2.
XX
PD   13-AUG-1998.
XX
PF   12-JAN-1998;   98WO-US000396.
XX
PR   06-FEB-1997;   97US-0038212P.
XX
PA   (HMRI ) HOECHST MARION ROUSSEL INC.
XX
PI   Linnik MD,  Racke MM,  Krakowsky JM,  Subramaniam A;
XX
DR   WPI; 1998-447224/38.
XX
PT   Compounds increasing transcription of endogenous human nerve growth
PT   factor - using vector containing the growth factor, for treating e.g.
PT   neurodegenerative diseases.
XX
PS   Example 8; Page 49; 89pp; English.
XX
CC   The sequence is that of a consensus binding motif found in human nerve
CC   growth factor (NGF) promoter regions. These can be used to screen for and
CC   characterise compounds able to modulate transcription from the hNGF
CC   promoters. Such compounds are useful in the treatment of e.g.
CC   neurodegenerative diseases. The compounds which modulate transcriptional
CC   activity of endogenous NGF promoters, especially in the brain, can more
CC   easily pass through the blood-brain barrier than exogenously administered
CC   NGF or fragments
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 4
AAV45242/c
ID   AAV45242 standard; DNA; 10 BP.
XX
AC   AAV45242;
XX
DT   09-NOV-1998  (first entry)
XX
DE   Human nerve growth factor exon promoter consensus binding motif.
XX
KW   NGF; nerve growth factor; treatment; promoter; neurodegenerative disease;
KW   consensus binding motif; ds.
XX
OS   Homo sapiens.
XX
PN   WO9835027-A2.
XX
PD   13-AUG-1998.
XX
PF   12-JAN-1998;   98WO-US000396.
XX
PR   06-FEB-1997;   97US-0038212P.
XX
PA   (HMRI ) HOECHST MARION ROUSSEL INC.
XX
PI   Linnik MD,  Racke MM,  Krakowsky JM,  Subramaniam A;
XX
DR   WPI; 1998-447224/38.
XX
PT   Compounds increasing transcription of endogenous human nerve growth
PT   factor - using vector containing the growth factor, for treating e.g.
PT   neurodegenerative diseases.
XX
PS   Example 8; Page 49; 89pp; English.
XX
CC   The sequence is that of a consensus binding motif found in human nerve
CC   growth factor (NGF) promoter regions. These can be used to screen for and
CC   characterise compounds able to modulate transcription from the hNGF
CC   promoters. Such compounds are useful in the treatment of e.g.
CC   neurodegenerative diseases. The compounds which modulate transcriptional
CC   activity of endogenous NGF promoters, especially in the brain, can more
CC   easily pass through the blood-brain barrier than exogenously administered
CC   NGF or fragments
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 5
AAV25510
ID   AAV25510 standard; DNA; 10 BP.
XX
AC   AAV25510;
XX
DT   09-JUL-1998  (first entry)
XX
DE   p53 binding site motif.
XX
KW   Human; bax promoter; apoptosis; autoimmune disease; cancer;
KW   Alzheimer's disease; Parkinson's disease; stroke; p53 binding site motif;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   US5744310-A.
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XX
PD   28-APR-1998.
XX
PF   29-JUL-1996;   96US-00688145.
XX
PR   29-JUL-1996;   96US-00688145.
XX
PA   (BURN-) BURNHAM INST.
XX
PI   Reed JC;
XX
DR   WPI; 1998-271064/24.
XX
PT   New bax gene promoter sequence(s) - are useful for identifying agents
PT   that regulate bax gene expression, e.g. to regulate apoptosis in tumour
PT   cells.
XX
PS   Example II; Col 31-32; 29pp; English.
XX
CC   The present p53 binding site motif can be found in the human bax
CC   promoter, i.e. nucleotides -3885 to -1 of the bax gene. Bax expression in
CC   a cell plays a central role in apoptosis. The control elements of the DNA
CC   encoding this protein are poorly understood. In certain autoimmune
CC   diseases, e.g. Alzheimer's or Parkinson's disease or strokes, a high
CC   level of cell death occurs and conversely in certain cancers, apoptosis
CC   is reduced. The promoter and its related molecules are useful for
CC   researching the rest of the controlling elements, and in assays for
CC   screening agents that can regulate bax activity
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 6
AAV25510/c
ID   AAV25510 standard; DNA; 10 BP.
XX
AC   AAV25510;
XX
DT   09-JUL-1998  (first entry)
XX
DE   p53 binding site motif.
XX
KW   Human; bax promoter; apoptosis; autoimmune disease; cancer;
KW   Alzheimer's disease; Parkinson's disease; stroke; p53 binding site motif;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   US5744310-A.
XX
PD   28-APR-1998.
XX
PF   29-JUL-1996;   96US-00688145.
XX
PR   29-JUL-1996;   96US-00688145.
XX
PA   (BURN-) BURNHAM INST.
XX
PI   Reed JC;
XX
DR   WPI; 1998-271064/24.
XX
PT   New bax gene promoter sequence(s) - are useful for identifying agents
PT   that regulate bax gene expression, e.g. to regulate apoptosis in tumour
PT   cells.
XX
PS   Example II; Col 31-32; 29pp; English.
XX
CC   The present p53 binding site motif can be found in the human bax
CC   promoter, i.e. nucleotides -3885 to -1 of the bax gene. Bax expression in
CC   a cell plays a central role in apoptosis. The control elements of the DNA
CC   encoding this protein are poorly understood. In certain autoimmune
CC   diseases, e.g. Alzheimer's or Parkinson's disease or strokes, a high
CC   level of cell death occurs and conversely in certain cancers, apoptosis
CC   is reduced. The promoter and its related molecules are useful for
CC   researching the rest of the controlling elements, and in assays for
CC   screening agents that can regulate bax activity
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 7
AAF31886
ID   AAF31886 standard; DNA; 10 BP.
XX
AC   AAF31886;
XX
DT   12-APR-2001  (first entry)
XX
DE   p53 binding site consensus sequence.
XX
KW   KARP-1; Ku86 autoantigen related protein; cancer; p53 binding site;
KW   immune deficiency disorder; biliary tract cancer; leucine zipper protein;
KW   cytostatic; immunosuppressant; gene therapy; KARP-1 inhibitor; ds.
XX
OS   Homo sapiens.
XX
PN   US6171857-B1.
XX
PD   09-JAN-2001.
XX
PF   16-OCT-1998;   98US-00173914.
XX
PR   17-OCT-1997;   97US-0064557P.
XX
PA   (UYBR-) UNIV BROWN RES FOUND.
XX
PI   Hendrickson EA;
XX
DR   WPI; 2001-146208/15.
XX
PT   Novel nucleic acids encoding leucine zipper protein, KARP-1 polypeptide,
PT   useful for treating cancer and immune deficiency disorder.
XX
PS   Example 10; Col 47; 61pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   Ku86 Autoantigen Related Protein (KARP-1) nucleic acid molecule. The KARP
CC   -1 nucleic acid and KARP-1 protein are useful for the treatment and/or
CC   diagnosis of diseases such as cancer and immune deficiency disorders.
CC   They are useful in combination with a KARP-1 inhibitor that inhibits
CC   double stranded DNA base repair. Inhibitors of KARP-1 are useful in the
CC   diagnosis or treatment of conditions characterised by the loss of KARP-1
CC   activity and in the treatment of cancer, e.g. biliary tract cancer
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 8
AAF31886/c
ID   AAF31886 standard; DNA; 10 BP.
XX
AC   AAF31886;
XX
DT   12-APR-2001  (first entry)
XX
DE   p53 binding site consensus sequence.
XX
KW   KARP-1; Ku86 autoantigen related protein; cancer; p53 binding site;
KW   immune deficiency disorder; biliary tract cancer; leucine zipper protein;
KW   cytostatic; immunosuppressant; gene therapy; KARP-1 inhibitor; ds.
XX
OS   Homo sapiens.
XX
PN   US6171857-B1.
XX
PD   09-JAN-2001.
XX
PF   16-OCT-1998;   98US-00173914.
XX
PR   17-OCT-1997;   97US-0064557P.
XX
PA   (UYBR-) UNIV BROWN RES FOUND.
XX
PI   Hendrickson EA;
XX
DR   WPI; 2001-146208/15.
XX
PT   Novel nucleic acids encoding leucine zipper protein, KARP-1 polypeptide,
PT   useful for treating cancer and immune deficiency disorder.
XX
PS   Example 10; Col 47; 61pp; English.
XX
CC   The present sequence is given in a specification relating to an isolated
CC   Ku86 Autoantigen Related Protein (KARP-1) nucleic acid molecule. The KARP
CC   -1 nucleic acid and KARP-1 protein are useful for the treatment and/or
CC   diagnosis of diseases such as cancer and immune deficiency disorders.
CC   They are useful in combination with a KARP-1 inhibitor that inhibits
CC   double stranded DNA base repair. Inhibitors of KARP-1 are useful in the
CC   diagnosis or treatment of conditions characterised by the loss of KARP-1
CC   activity and in the treatment of cancer, e.g. biliary tract cancer
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 9
AAF58009
ID   AAF58009 standard; DNA; 10 BP.
XX
AC   AAF58009;
XX
DT   26-APR-2001  (first entry)
XX
DE   Wild-type p53 binding consensus sequence.
XX
KW   Bacterial toxin; antidote; cell death; apoptosis; developmental control;
KW   organogenesis; cancer; psoriasis; arteriosclerosis; knock-out;
KW   seedless fruit; male sterility; proteic killer gene system; ds.
XX
OS   Unidentified.
XX
PN   WO200105421-A1.
XX
PD   25-JAN-2001.
XX
PF   17-JUL-2000; 2000WO-GB002743.
XX
PR   16-JUL-1999;   99GB-00016810.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   De La Cueva Mendez G,  Laskey RA,  Mills AD,  Diaz Orejas R;
XX
DR   WPI; 2001-182641/18.
XX
PT   Inhibiting cell proliferation and/or cell cycle progression used for
PT   treating tumors, cancer and psoriasis, involves using toxins and
PT   toxin/antidote system based on bacterial system.
XX
PS   Disclosure; Page 27; 64pp; English.
XX
CC   The present invention describes a method of inhibiting cell proliferation
CC   or cell cycle progression, involving providing eukaryotic cells with a
CC   bacterial toxin and an antidote to said toxin under appropriate control
CC   for selective cell cycle inhibition or killing of target cells. This is
CC   useful in the treatment of cancer, arteriosclerosis, psoriasis and other
CC   hyperproliferative diseases, in the production of male sterile, seedless
CC   and disease resistant plants, and in the production of animal knock-outs
CC   which enable the study of organogenesis and developmental control. The
CC   present sequence is the p53 binding sequence which is described in the
CC   specification
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 10
AAF58009/c
ID   AAF58009 standard; DNA; 10 BP.
XX
AC   AAF58009;
XX
DT   26-APR-2001  (first entry)
XX
DE   Wild-type p53 binding consensus sequence.
XX
KW   Bacterial toxin; antidote; cell death; apoptosis; developmental control;
KW   organogenesis; cancer; psoriasis; arteriosclerosis; knock-out;
KW   seedless fruit; male sterility; proteic killer gene system; ds.
XX
OS   Unidentified.
XX
PN   WO200105421-A1.
XX
PD   25-JAN-2001.
XX
PF   17-JUL-2000; 2000WO-GB002743.
XX
PR   16-JUL-1999;   99GB-00016810.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   De La Cueva Mendez G,  Laskey RA,  Mills AD,  Diaz Orejas R;
```

XX
DR WPI; 2001-182641/18.
XX
PT Inhibiting cell proliferation and/or cell cycle progression used for
PT treating tumors, cancer and psoriasis, involves using toxins and
PT toxin/antidote system based on bacterial system.
XX
PS Disclosure; Page 27; 64pp; English.
XX
CC The present invention describes a method of inhibiting cell proliferation
CC or cell cycle progression, involving providing eukaryotic cells with a
CC bacterial toxin and an antidote to said toxin under appropriate control
CC for selective cell cycle inhibition or killing of target cells. This is
CC useful in the treatment of cancer, arteriosclerosis, psoriasis and other
CC hyperproliferative diseases, in the production of male sterile, seedless
CC and disease resistant plants, and in the production of animal knock-outs
CC which enable the study of organogenesis and developmental control. The
CC present sequence is the p53 binding sequence which is described in the
CC specification
XX
SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

Query Match 100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWWGYYY 10
||||||||||
Db 10 RRRCWWGYYY 1

RESULT 11
ACA62195
ID ACA62195 standard; DNA; 10 BP.
XX
AC ACA62195;
XX
DT 08-AUG-2003 (first entry)
XX
DE Consensus p53 recognition sequence.
XX
KW p53; ds; genome instability disease; cancer; DNA binding factor;
KW proximity-based luminescence detection.
XX
OS Synthetic.
XX
PN US2003049625-A1.
XX
PD 13-MAR-2003.
XX
PF 13-AUG-2001; 2001US-00928385.
XX
PR 13-AUG-2001; 2001US-00928385.
XX
PA (UYSL-) UNIV SAINT LOUIS.
XX
PI Heyduk T;
XX
DR WPI; 2003-456598/43.
XX
PT Detecting or quantifying sample DNA binding factors, or determining
PT activity of DNA binding factor, by detecting binding of DNA binding
PT factor with DNA binding element by proximity-based luminescence
PT detection.
XX
PS Example 8; Page 15; 43pp; English.
XX
CC The invention relates to a method of detecting/quantifying DNA binding
CC factors in a sample, or determining activity of DNA binding factors,
CC involves combining two sets of nucleic acid components (NCs) with sample,
CC where each NC comprises DNA binding element (DE), one NC is labelled with
CC fluorescence donor and other NC labeled with fluorescence acceptor, to
CC emit light at unique wavelength and detecting DNA binding factors-DE
CC binding by proximity-based luminescence detection. The method is useful
CC for detecting or quantifying DNA binding factors in a sample and for
CC determining the activity of DNA binding factor. The method is useful for
CC determining the amount of an analyte in a sample, where the association
CC of DNA binding factors and DE is mediated by the analyte e.g. secondary
CC messenger molecule (e.g. cAMP), cellular event, drug agent, reagent,
CC prospective drug, prospective agent and prospective reagent. The method
CC is also useful for diagnosing a disease mediated by a DNA binding factor
CC in a human patient who is suffering from a type of cancer or disease of
CC genome instability. The methods are useful for detecting mediating
CC analytes, to diagnose diseases, and/or to screen for drugs that mediate
CC the activity of DNA binding factors. The method is inexpensive, simple
CC and is compatible with high-throughput detection formats. The present
CC sequence represents the consensus p53 recognition sequence
XX
SQ Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

Query Match 100.0%; Score 10; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWWGYYY 10
||||||||||
Db 1 RRRCWWGYYY 10

RESULT 12
ACA62195/c
ID ACA62195 standard; DNA; 10 BP.
XX
AC ACA62195;
XX
DT 08-AUG-2003 (first entry)
XX
DE Consensus p53 recognition sequence.
XX
KW p53; ds; genome instability disease; cancer; DNA binding factor;
KW proximity-based luminescence detection.
XX
OS Synthetic.
XX
PN US2003049625-A1.
XX
PD 13-MAR-2003.
XX
PF 13-AUG-2001; 2001US-00928385.
XX
PR 13-AUG-2001; 2001US-00928385.
XX
PA (UYSL-) UNIV SAINT LOUIS.
XX
PI Heyduk T;
XX
DR WPI; 2003-456598/43.
XX
PT Detecting or quantifying sample DNA binding factors, or determining
PT activity of DNA binding factor, by detecting binding of DNA binding
PT factor with DNA binding element by proximity-based luminescence
PT detection.
XX
PS Example 8; Page 15; 43pp; English.
XX
CC The invention relates to a method of detecting/quantifying DNA binding
CC factors in a sample, or determining activity of DNA binding factors,
CC involves combining two sets of nucleic acid components (NCs) with sample,
CC where each NC comprises DNA binding element (DE), one NC is labelled with
CC fluorescence donor and other NC labeled with fluorescence acceptor, to
CC emit light at unique wavelength and detecting DNA binding factors-DE
CC binding by proximity-based luminescence detection. The method is useful
CC for detecting or quantifying DNA binding factors in a sample and for
CC determining the activity of DNA binding factor. The method is useful for
CC determining the amount of an analyte in a sample, where the association
CC of DNA binding factors and DE is mediated by the analyte e.g. secondary

```
CC   messenger molecule (e.g. cAMP), cellular event, drug agent, reagent,
CC   prospective drug, prospective agent and prospective reagent. The method
CC   is also useful for diagnosing a disease mediated by a DNA binding factor
CC   in a human patient who is suffering from a type of cancer or disease of
CC   genome instability. The methods are useful for detecting mediating
CC   analytes, to diagnose diseases, and/or to screen for drugs that mediate
CC   the activity of DNA binding factors. The method is inexpensive, simple
CC   and is compatible with high-throughput detection formats. The present
CC   sequence represents the consensus p53 recognition sequence
XX
SQ   Sequence 10 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 8 Other;

  Query Match             100.0%;  Score 10;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 1


RESULT 13
ABK91337
ID   ABK91337 standard; DNA; 19 BP.
XX
AC   ABK91337;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human JFY1, p53-binding site, CBS.
XX
KW   Human; JFY1; apoptosis; cancer; cellular proliferation; p53;
KW   gene therapy; neoplastic cancer cell; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200264790-A2.
XX
PD   22-AUG-2002.
XX
PF   12-DEC-2001; 2001WO-US047455.
XX
PR   19-DEC-2000; 2000US-0256328P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Yu J,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2002-643485/69.
XX
PT   New JFY1 proteins and nucleic acids, useful for inducing rapid apoptosis
PT   in cancer cells, for treating cancers or other diseases characterized by
PT   unwanted cellular proliferation, and as a substitute for p53 in cancer
PT   gene therapy.
XX
PS   Disclosure; Fig 3; 45pp; English.
XX
CC   The invention relates to an isolated and purified JFY1 coding sequence
CC   and purified JFY1 protein. The JFY1 polynucleotide is useful for inducing
CC   rapid apoptosis in cancer cells, for treating cancers or other diseases
CC   characterised by unwanted cellular proliferation, and as a substitute for
CC   p53 in cancer gene therapy. The expression product of JFY1 may be used as
CC   an indicator for neoplastic cancer cells and in determining the prognosis
CC   of a cancer patient. The present sequence represents a human JFY1, p53-
CC   binding site
XX
SQ   Sequence 19 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 15 Other;

  Query Match             100.0%;  Score 10;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         10 RRRCWWGYYY 19


RESULT 14
ABK91337/c
ID   ABK91337 standard; DNA; 19 BP.
XX
AC   ABK91337;
XX
DT   15-NOV-2002  (first entry)
XX
DE   Human JFY1, p53-binding site, CBS.
XX
KW   Human; JFY1; apoptosis; cancer; cellular proliferation; p53;
KW   gene therapy; neoplastic cancer cell; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200264790-A2.
XX
PD   22-AUG-2002.
XX
PF   12-DEC-2001; 2001WO-US047455.
XX
PR   19-DEC-2000; 2000US-0256328P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Yu J,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2002-643485/69.
XX
PT   New JFY1 proteins and nucleic acids, useful for inducing rapid apoptosis
PT   in cancer cells, for treating cancers or other diseases characterized by
PT   unwanted cellular proliferation, and as a substitute for p53 in cancer
PT   gene therapy.
XX
PS   Disclosure; Fig 3; 45pp; English.
XX
CC   The invention relates to an isolated and purified JFY1 coding sequence
CC   and purified JFY1 protein. The JFY1 polynucleotide is useful for inducing
CC   rapid apoptosis in cancer cells, for treating cancers or other diseases
CC   characterised by unwanted cellular proliferation, and as a substitute for
CC   p53 in cancer gene therapy. The expression product of JFY1 may be used as
CC   an indicator for neoplastic cancer cells and in determining the prognosis
CC   of a cancer patient. The present sequence represents a human JFY1, p53-
CC   binding site
XX
SQ   Sequence 19 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 15 Other;

  Query Match             100.0%;  Score 10;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         19 RRRCWWGYYY 10


RESULT 15
AAZ51676
ID   AAZ51676 standard; DNA; 20 BP.
XX
AC   AAZ51676;
XX
DT   21-JUN-2000  (first entry)
XX
DE   Human p53-responsive element consensus sequence.
XX
KW   PRG; p53 target; human; p53-responsive element; cell proliferation;
```

KW consensus; immunomodulatory; cytostatic; gene therapy; inducer; cancer;
KW tumour cell; diagnosis; therapeutic; proliferative disease; apoptosis;
KW cell cycle arrest; modulate; treatment; knockout animal;
KW cancer susceptibility; ds.
XX
OS Homo sapiens.
XX
PN WO200012526-A1.
XX
PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-US019551.
XX
PR 28-AUG-1998; 98US-0098251P.
XX
PA (UYPR-) UNIV PRINCETON.
XX
PI Horikoshi N, Shenk T;
XX
DR WPI; 2000-246724/21.
XX
PT New p53-inducible isolated nucleic acid molecule including open reading
PT frame encoding human homolog of Drosophila melanogaster peroxidasin,
PT useful e.g. in detection and treatment of cancer.
XX
PS Example 2; Page 78; 83pp; English.
XX
CC The present sequence is the p53-responsive element consensus sequence,
CC located on PRG target molecules, that are modulated on induction by p53
CC activity. The tumour suppressor gene p53, functions as a transcription
CC factor and interacts with this responsive element and activates
CC transcription from the promoter. PRG sequences are potential targets of
CC p53 regulatory activity and are useful for modulation of cellular
CC proliferation. It has cytostatic and immunomodulatory activity. PRG
CC polynucleotides, proteins and antibodies are useful as diagnostic and
CC therapeutic agents for detection and treatment of cancer and other
CC proliferative diseases. The gene/cDNA may be used for gene therapy, to
CC restore a gene function downstream of p53, that cannot be activated in
CC the p53-deficient tumour cell. Antibodies can be used as inducers of cell
CC cycle arrest and/or apoptosis. The DNA sequences can be used to generate
CC 'knockout' animals as a model of cancer susceptibility
XX
SQ Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;

Query Match 100.0%; Score 10; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWWGYYY 10
||||||||||
Db 1 RRRCWWGYYY 10

RESULT 16
AAZ51676/c
ID AAZ51676 standard; DNA; 20 BP.
XX
AC AAZ51676;
XX
DT 21-JUN-2000 (first entry)
XX
DE Human p53-responsive element consensus sequence.
XX
KW PRG; p53 target; human; p53-responsive element; cell proliferation;
KW consensus; immunomodulatory; cytostatic; gene therapy; inducer; cancer;
KW tumour cell; diagnosis; therapeutic; proliferative disease; apoptosis;
KW cell cycle arrest; modulate; treatment; knockout animal;
KW cancer susceptibility; ds.
XX
OS Homo sapiens.
XX
PN WO200012526-A1.
XX
PD 09-MAR-2000.
XX
PF 27-AUG-1999; 99WO-US019551.
XX
PR 28-AUG-1998; 98US-0098251P.
XX
PA (UYPR-) UNIV PRINCETON.
XX
PI Horikoshi N, Shenk T;
XX
DR WPI; 2000-246724/21.
XX
PT New p53-inducible isolated nucleic acid molecule including open reading
PT frame encoding human homolog of Drosophila melanogaster peroxidasin,
PT useful e.g. in detection and treatment of cancer.
XX
PS Example 2; Page 78; 83pp; English.
XX
CC The present sequence is the p53-responsive element consensus sequence,
CC located on PRG target molecules, that are modulated on induction by p53
CC activity. The tumour suppressor gene p53, functions as a transcription
CC factor and interacts with this responsive element and activates
CC transcription from the promoter. PRG sequences are potential targets of
CC p53 regulatory activity and are useful for modulation of cellular
CC proliferation. It has cytostatic and immunomodulatory activity. PRG
CC polynucleotides, proteins and antibodies are useful as diagnostic and
CC therapeutic agents for detection and treatment of cancer and other
CC proliferative diseases. The gene/cDNA may be used for gene therapy, to
CC restore a gene function downstream of p53, that cannot be activated in
CC the p53-deficient tumour cell. Antibodies can be used as inducers of cell
CC cycle arrest and/or apoptosis. The DNA sequences can be used to generate
CC 'knockout' animals as a model of cancer susceptibility
XX
SQ Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;

Query Match 100.0%; Score 10; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWWGYYY 10
||||||||||
Db 20 RRRCWWGYYY 11

RESULT 17
AAL42021
ID AAL42021 standard; DNA; 20 BP.
XX
AC AAL42021;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human generic p53 DNA binding site consensus sequence.
XX
KW Human; generic p53 DNA binding site consensus sequence; ss;
KW chromosomal immunoprecipitation; Chip; target gene discovery;
KW coding sequence discovery; regulatory element discovery;
KW transcription factor discovery; screening; highly automatable;
KW high-throughput analysis.
XX
OS Homo sapiens.
XX
PN WO200214550-A2.
XX
PD 21-FEB-2002.
XX
PF 08-AUG-2001; 2001WO-US024823.
XX
PR 14-AUG-2000; 2000US-0225225P.
XX
PA (TRAN-) TRANSGENETICS INC.
XX
PI Burgess RM, Lunyak V, Noskin L;

```
XX
DR   WPI; 2002-241911/29.
XX
PT   Utilizing sequential chromosomal immunoprecipitation for discovery and
PT   characterization of target genes for transcription factors which are of
PT   DNA binding nature.
XX
PS   Example; Page 47; 68pp; English.
XX
CC   The invention comprises a method which utilises chromosomal
CC   immunoprecipitation (Chip) procedures for the discovery and
CC   characterisation of transcription factor target genes. The method of the
CC   invention is useful for the discovery and characterisation of
CC   transcription factor target genes. The method is preferably useful for
CC   the discovery and characterisation of: target genes (e.g. coding
CC   sequences and regulatory elements); and DNA binding transcription
CC   factors. The DNA sequences isolated by the method of the invention are
CC   useful for cross-hybridising against libraries of nucleotide sequences,
CC   and for screening against arrays of nucleotide sequences. The method of
CC   the invention is highly automatable, allowing for extensive high-
CC   throughput analysis of virtually any genetic cascade. The present DNA
CC   sequence represents a generic p53 DNA binding site consensus sequence
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;

  Query Match             100.0%;  Score 10;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 18
AAL42021/c
ID   AAL42021 standard; DNA; 20 BP.
XX
AC   AAL42021;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Human generic p53 DNA binding site consensus sequence.
XX
KW   Human; generic p53 DNA binding site consensus sequence; ss;
KW   chromosomal immunoprecipitation; Chip; target gene discovery;
KW   coding sequence discovery; regulatory element discovery;
KW   transcription factor discovery; screening; highly automatable;
KW   high-throughput analysis.
XX
OS   Homo sapiens.
XX
PN   WO200214550-A2.
XX
PD   21-FEB-2002.
XX
PF   08-AUG-2001; 2001WO-US024823.
XX
PR   14-AUG-2000; 2000US-0225225P.
XX
PA   (TRAN-) TRANSGENETICS INC.
XX
PI   Burgess RM,  Lunyak V,  Noskin L;
XX
DR   WPI; 2002-241911/29.
XX
PT   Utilizing sequential chromosomal immunoprecipitation for discovery and
PT   characterization of target genes for transcription factors which are of
PT   DNA binding nature.
XX
PS   Example; Page 47; 68pp; English.
XX
CC   The invention comprises a method which utilises chromosomal
CC   immunoprecipitation (Chip) procedures for the discovery and
CC   characterisation of transcription factor target genes. The method of the
CC   invention is useful for the discovery and characterisation of
CC   transcription factor target genes. The method is preferably useful for
CC   the discovery and characterisation of: target genes (e.g. coding
CC   sequences and regulatory elements); and DNA binding transcription
CC   factors. The DNA sequences isolated by the method of the invention are
CC   useful for cross-hybridising against libraries of nucleotide sequences,
CC   and for screening against arrays of nucleotide sequences. The method of
CC   the invention is highly automatable, allowing for extensive high-
CC   throughput analysis of virtually any genetic cascade. The present DNA
CC   sequence represents a generic p53 DNA binding site consensus sequence
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;

  Query Match             100.0%;  Score 10;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         20 RRRCWWGYYY 11


RESULT 19
AAD30357
ID   AAD30357 standard; DNA; 20 BP.
XX
AC   AAD30357;
XX
DT   21-MAY-2002  (first entry)
XX
DE   p53 consensus binding site DNA.
XX
KW   Testes-specific, vespid and pathogenic protein; RTVP; therapy;
KW   anti-neoplastic; prostatic neoplasia; prostate carcinoma; cytokine;
KW   metastatic disease; neoplastic disease; immune system; growth factor;
KW   cytostatic; ds.
XX
OS   Unidentified.
XX
PN   WO200206344-A2.
XX
PD   24-JAN-2002.
XX
PF   08-JUN-2001; 2001WO-US018487.
XX
PR   08-JUN-2000; 2000US-0209989P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Thompson TC,  Ren C;
XX
DR   WPI; 2002-195804/25.
XX
PT   Novel testes-specific, vespid and pathogenic polypeptide useful for
PT   treating and preventing prostatic neoplastic diseases, such as prostatic
PT   carcinoma and metastatic carcinoma, has antineoplastic activity.
XX
PS   Example 1; Page 16; 72pp; English.
XX
CC   The invention relates to a gene encoding non-human testes-specific,
CC   vespid and pathogenic protein (RTVP) having anti-neoplastic activity. The
CC   invention further relates to compositions and methods based on RTVP for
CC   the treatment, prevention and detection of prostatic neoplasia such as
CC   prostate carcinoma and associated metastatic disease. Diagnostic kit
CC   comprising RTVP protein is useful for the detection of neoplastic
CC   disease. Composition comprising RTVP protein is useful in the diagnosis,
CC   studying and treatment of prostatic neoplasia such as prostatic carcinoma
CC   and associated metastatic disease. It is also useful for stimulating
CC   immune system e.g. cytokines and growth factors in a patient. The present
CC   sequence is p53 consensus binding site DNA used in the identification of
CC   mRTVP-1 as a p53 target gene
```

```
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;

  Query Match            100.0%;  Score 10;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 20
AAD30357/c
ID   AAD30357 standard; DNA; 20 BP.
XX
AC   AAD30357;
XX
DT   21-MAY-2002  (first entry)
XX
DE   p53 consensus binding site DNA.
XX
KW   Testes-specific, vespid and pathogenic protein; RTVP; therapy;
KW   anti-neoplastic; prostatic neoplasia; prostate carcinoma; cytokine;
KW   metastatic disease; neoplastic disease; immune system; growth factor;
KW   cytostatic; ds.
XX
OS   Unidentified.
XX
PN   WO200206344-A2.
XX
PD   24-JAN-2002.
XX
PF   08-JUN-2001; 2001WO-US018487.
XX
PR   08-JUN-2000; 2000US-0209989P.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   Thompson TC,  Ren C;
XX
DR   WPI; 2002-195804/25.
XX
PT   Novel testes-specific, vespid and pathogenic polypeptide useful for
PT   treating and preventing prostatic neoplastic diseases, such as prostatic
PT   carcinoma and metastatic carcinoma, has antineoplastic activity.
XX
PS   Example 1; Page 16; 72pp; English.
XX
CC   The invention relates to a gene encoding non-human testes-specific,
CC   vespid and pathogenic protein (RTVP) having anti-neoplastic activity. The
CC   invention further relates to compositions and methods based on RTVP for
CC   the treatment, prevention and detection of prostatic neoplasia such as
CC   prostate carcinoma and associated metastatic disease. Diagnostic kit
CC   comprising RTVP protein is useful for the detection of neoplastic
CC   disease. Composition comprising RTVP protein is useful in the diagnosis,
CC   studying and treatment of prostatic neoplasia such as prostatic carcinoma
CC   and associated metastatic disease. It is also useful for stimulating
CC   immune system e.g. cytokines and growth factors in a patient. The present
CC   sequence is p53 consensus binding site DNA used in the identification of
CC   mRTVP-1 as a p53 target gene
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;

  Query Match            100.0%;  Score 10;  DB 6;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         20 RRRCWWGYYY 11


RESULT 21
ADC71586
ID   ADC71586 standard; DNA; 20 BP.
XX
AC   ADC71586;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Degenerate nucleotide Seq ID16 related to apoptosis induction.
XX
KW   apoptosis; p53; p73; heterooligomer; deltaNp73; cytostatic;
KW   p73 transcription; p53 transcription; cancer; neuroblastoma; ss.
XX
OS   Unidentified.
XX
PN   WO2003061710-A1.
XX
PD   31-JUL-2003.
XX
PF   23-JAN-2003; 2003WO-JP000605.
XX
PR   25-JAN-2002; 2002JP-00017486.
XX
PA   (HISM ) HISAMITSU PHARM CO LTD.
PA   (CHIB-) CHIBA PREFECTURE.
XX
PI   Nakagawara A;
XX
DR   WPI; 2003-598710/56.
XX
PT   Regulators of apoptosis induction by p53 or p73 for treatment and
PT   prevention of neuroblastoma and other cancers.
XX
PS   Example 3; SEQ ID NO 16; 65pp; Japanese.
XX
CC   This invention relates to novel agents which regulate the induction of
CC   apoptosis by p53 or p73 by formation of a heterooligomer with deltaNp73.
CC   The invention may have cytostatic activity by acting as an agonist or
CC   antagonist of p73 and p53 transcription. Agents which regulate the
CC   induction of apoptosis by p53 or p73 are useful for treatment and
CC   prevention of cancer, including neuroblastoma. The present sequence is
CC   that of a degenerate DNA sequence which is related to the invention.
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;

  Query Match            100.0%;  Score 10;  DB 10;  Length 20;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 22
ADC71586/c
ID   ADC71586 standard; DNA; 20 BP.
XX
AC   ADC71586;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Degenerate nucleotide Seq ID16 related to apoptosis induction.
XX
KW   apoptosis; p53; p73; heterooligomer; deltaNp73; cytostatic;
KW   p73 transcription; p53 transcription; cancer; neuroblastoma; ss.
XX
OS   Unidentified.
XX
PN   WO2003061710-A1.
XX
PD   31-JUL-2003.
XX
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PF   23-JAN-2003; 2003WO-JP000605.
XX
PR   25-JAN-2002; 2002JP-00017486.
XX
PA   (HISM ) HISAMITSU PHARM CO LTD.
PA   (CHIB-) CHIBA PREFECTURE.
XX
PI   Nakagawara A;
XX
DR   WPI; 2003-598710/56.
XX
PT   Regulators of apoptosis induction by p53 or p73 for treatment and
PT   prevention of neuroblastoma and other cancers.
XX
PS   Example 3; SEQ ID NO 16; 65pp; Japanese.
XX
CC   This invention relates to novel agents which regulate the induction of
CC   apoptosis by p53 or p73 by formation of a heterooligomer with deltaNp73.
CC   The invention may have cytostatic activity by acting as an agonist or
CC   antagonist of p73 and p53 transcription. Agents which regulate the
CC   induction of apoptosis by p53 or p73 are useful for treatment and
CC   prevention of cancer, including neuroblastoma. The present sequence is
CC   that of a degenerate DNA sequence which is related to the invention.
XX
SQ   Sequence 20 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 16 Other;

  Query Match             100.0%;  Score 10;  DB 10;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         20 RRRCWWGYYY 11


RESULT 23
AAZ51677
ID   AAZ51677 standard; DNA; 21 BP.
XX
AC   AAZ51677;
XX
DT   21-JUN-2000  (first entry)
XX
DE   Human p53 binding consensus sequence.
XX
KW   PRG; p53 target; human; p53-responsive element; cell proliferation;
KW   consensus; immunomodulatory; cytostatic; gene therapy; inducer; cancer;
KW   tumour cell; diagnosis; therapeutic; proliferative disease; apoptosis;
KW   cell cycle arrest; modulate; treatment; knockout animal;
KW   cancer susceptibility; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    11
FT                   /*tag=  a
FT                   /note= "n can be 1-10 nucleotides"
XX
PN   WO200012526-A1.
XX
PD   09-MAR-2000.
XX
PF   27-AUG-1999;   99WO-US019551.
XX
PR   28-AUG-1998;   98US-0098251P.
XX
PA   (UYPR-) UNIV PRINCETON.
XX
PI   Horikoshi N,  Shenk T;
XX
DR   WPI; 2000-246724/21.
XX
PT   New p53-inducible isolated nucleic acid molecule including open reading
PT   frame encoding human homolog of Drosophila melanogaster peroxidasin,
PT   useful e.g. in detection and treatment of cancer.
XX
PS   Example 2; Page 78; 83pp; English.
XX
CC   The present sequence is the p53 binding consensus sequence, constructed
CC   from the five potential p53 responsive elements (A-E), located on PRG
CC   target molecules. They are modulated on induction by p53 activity. The
CC   tumour suppressor gene p53, functions as a transcription factor and
CC   interacts with this responsive element and activates transcription from
CC   the promoter. PRG sequences are potential targets of p53 regulatory
CC   activity and are useful for modulation of cellular proliferation. It has
CC   cytostatic and immunomodulatory activity. PRG polynucleotides, proteins
CC   and antibodies are useful as diagnostic and therapeutic agents for
CC   detection and treatment of cancer and other proliferative diseases. The
CC   gene/cDNA may be used for gene therapy, to restore a gene function
CC   downstream of p53, that cannot be activated in the p53-deficient tumour
CC   cell. Antibodies can be used as inducers of cell cycle arrest and/or
CC   apoptosis. The DNA sequences can be used to generate 'knockout' animals
CC   as a model of cancer susceptibility
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 17 Other;

  Query Match             100.0%;  Score 10;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db          1 RRRCWWGYYY 10


RESULT 24
AAZ51677/c
ID   AAZ51677 standard; DNA; 21 BP.
XX
AC   AAZ51677;
XX
DT   21-JUN-2000  (first entry)
XX
DE   Human p53 binding consensus sequence.
XX
KW   PRG; p53 target; human; p53-responsive element; cell proliferation;
KW   consensus; immunomodulatory; cytostatic; gene therapy; inducer; cancer;
KW   tumour cell; diagnosis; therapeutic; proliferative disease; apoptosis;
KW   cell cycle arrest; modulate; treatment; knockout animal;
KW   cancer susceptibility; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    11
FT                   /*tag=  a
FT                   /note= "n can be 1-10 nucleotides"
XX
PN   WO200012526-A1.
XX
PD   09-MAR-2000.
XX
PF   27-AUG-1999;   99WO-US019551.
XX
PR   28-AUG-1998;   98US-0098251P.
XX
PA   (UYPR-) UNIV PRINCETON.
XX
PI   Horikoshi N,  Shenk T;
XX
DR   WPI; 2000-246724/21.
XX
PT   New p53-inducible isolated nucleic acid molecule including open reading
PT   frame encoding human homolog of Drosophila melanogaster peroxidasin,
PT   useful e.g. in detection and treatment of cancer.
XX
```

```
PS   Example 2; Page 78; 83pp; English.
XX
CC   The present sequence is the p53 binding consensus sequence, constructed
CC   from the five potential p53 responsive elements (A-E), located on PRG
CC   target molecules. They are modulated on induction by p53 activity. The
CC   tumour suppressor gene p53, functions as a transcription factor and
CC   interacts with this responsive element and activates transcription from
CC   the promoter. PRG sequences are potential targets of p53 regulatory
CC   activity and are useful for modulation of cellular proliferation. It has
CC   cytostatic and immunomodulatory activity. PRG polynucleotides, proteins
CC   and antibodies are useful as diagnostic and therapeutic agents for
CC   detection and treatment of cancer and other proliferative diseases. The
CC   gene/cDNA may be used for gene therapy, to restore a gene function
CC   downstream of p53, that cannot be activated in the p53-deficient tumour
CC   cell. Antibodies can be used as inducers of cell cycle arrest and/or
CC   apoptosis. The DNA sequences can be used to generate 'knockout' animals
CC   as a model of cancer susceptibility
XX
SQ   Sequence 21 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 17 Other;

  Query Match             100.0%;  Score 10;  DB 3;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRCWWGYYY 10
              ||||||||||
Db         21 RRRCWWGYYY 12


RESULT 25
AAQ56429
ID   AAQ56429 standard; DNA; 20 BP.
XX
AC   AAQ56429;
XX
DT   25-MAR-2003  (revised)
DT   29-JUL-1994  (first entry)
XX
DE   E6 consensus negative strand primer WD163.
XX
KW   Human papilloma virus; amplification; polymerase chain reaction; PCR;
KW   detection; assay; genital; ss.
XX
OS   Synthetic.
XX
PN   US5283171-A.
XX
PD   01-FEB-1994.
XX
PF   15-FEB-1991;   91US-00651356.
XX
PR   09-SEP-1988;   88US-00243486.
PR   10-MAR-1989;   89US-00322550.
PR   29-AUG-1989;   89WO-US003747.
XX
PA   (UYRP ) UNIV ROCHESTER.
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Wolinsky SM,  Broker TR,  Ting Y,  Manos MM,  Wright DK;
XX
DR   WPI; 1994-048082/06.
XX
PT   Detection of genital human papilloma virus - by PCR amplification using
PT   defined consensus primer pairs.
XX
PS   Disclosure; Page 9; 13pp; English.
XX
CC   The sequence is that of the human papilloma virus (HPV) E6 consensus
CC   negative strand primer WD163 which was used in the amplification by PCR
CC   of HPV DNA. It may be used as part of a simple and rapid assay method for
CC   detecting and typing HPV in biological samples. (Updated on 25-MAR-2003
CC   to correct PF field.)
XX
SQ   Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;

  Query Match             50.0%;  Score 5;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWGYY 9
              |||||
Db         11 WWGYY 15


RESULT 26
AAQ56429/c
ID   AAQ56429 standard; DNA; 20 BP.
XX
AC   AAQ56429;
XX
DT   25-MAR-2003  (revised)
DT   29-JUL-1994  (first entry)
XX
DE   E6 consensus negative strand primer WD163.
XX
KW   Human papilloma virus; amplification; polymerase chain reaction; PCR;
KW   detection; assay; genital; ss.
XX
OS   Synthetic.
XX
PN   US5283171-A.
XX
PD   01-FEB-1994.
XX
PF   15-FEB-1991;   91US-00651356.
XX
PR   09-SEP-1988;   88US-00243486.
PR   10-MAR-1989;   89US-00322550.
PR   29-AUG-1989;   89WO-US003747.
XX
PA   (UYRP ) UNIV ROCHESTER.
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Wolinsky SM,  Broker TR,  Ting Y,  Manos MM,  Wright DK;
XX
DR   WPI; 1994-048082/06.
XX
PT   Detection of genital human papilloma virus - by PCR amplification using
PT   defined consensus primer pairs.
XX
PS   Disclosure; Page 9; 13pp; English.
XX
CC   The sequence is that of the human papilloma virus (HPV) E6 consensus
CC   negative strand primer WD163 which was used in the amplification by PCR
CC   of HPV DNA. It may be used as part of a simple and rapid assay method for
CC   detecting and typing HPV in biological samples. (Updated on 25-MAR-2003
CC   to correct PF field.)
XX
SQ   Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;

  Query Match             50.0%;  Score 5;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRCWW 6
              |||||
Db         15 RRCWW 11


RESULT 27
AAT44825
ID   AAT44825 standard; DNA; 20 BP.
XX
AC   AAT44825;
XX
DT   25-MAR-2003  (revised)
```

```
DT   31-JAN-1997  (first entry)
XX
DE   HPV E6 region negative strand primer WD163.
XX
KW   Probe; primer; PCR; polymerase chain reaction; amplification;
KW   human papillomavirus; consensus; ss.
XX
OS   Synthetic.
XX
PN   US5527898-A.
XX
PD   18-JUN-1996.
XX
PF   07-JUN-1995;   95US-00474542.
XX
PR   09-SEP-1988;   88US-00243486.
PR   10-MAR-1989;   89US-00322550.
PR   09-SEP-1989;   89WO-US003747.
PR   14-NOV-1990;   90US-00613142.
PR   20-APR-1993;   93US-00050743.
PR   24-SEP-1993;   93US-00126452.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Bauer HM,  Resnick RM,  Greer CE,  Manos MM,  Zhang TY,  Gravitt PE;
XX
DR   WPI; 1996-299903/30.
XX
PT   Nucleic acid hybridisation probes - specific for selected human papilloma
PT   virus types.
XX
PS   Disclosure; Col 37-38; 96pp; English.
XX
CC   The invention relates to new oligonucleotide probes and primers used for
CC   the detection of human papillomaviruses (HPV) which are not genital types
CC   6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
CC   to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC   primers can be used to detect these HPV types in conjunction with the
CC   consensus primers and typing probes AAT44733-T44906, which are based on
CC   and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC   sequences. Detection of the amplification prods. is done with probes
CC   derived from consensus sequences found in all characterised HPV
CC   sequences. The negative strand primers AAT44821-6 are used with positive
CC   strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
CC   the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
CC   are detected using the E6 consensus probes AAT44839-40, specific for
CC   these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;

  Query Match             50.0%;  Score 5;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWGYY 9
              |||||
Db         11 WWGYY 15


RESULT 28
AAT44825/c
ID   AAT44825 standard; DNA; 20 BP.
XX
AC   AAT44825;
XX
DT   25-MAR-2003  (revised)
DT   31-JAN-1997  (first entry)
XX
DE   HPV E6 region negative strand primer WD163.
XX
KW   Probe; primer; PCR; polymerase chain reaction; amplification;
KW   human papillomavirus; consensus; ss.
XX
OS   Synthetic.
XX
PN   US5527898-A.
XX
PD   18-JUN-1996.
XX
PF   07-JUN-1995;   95US-00474542.
XX
PR   09-SEP-1988;   88US-00243486.
PR   10-MAR-1989;   89US-00322550.
PR   09-SEP-1989;   89WO-US003747.
PR   14-NOV-1990;   90US-00613142.
PR   20-APR-1993;   93US-00050743.
PR   24-SEP-1993;   93US-00126452.
XX
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Bauer HM,  Resnick RM,  Greer CE,  Manos MM,  Zhang TY,  Gravitt PE;
XX
DR   WPI; 1996-299903/30.
XX
PT   Nucleic acid hybridisation probes - specific for selected human papilloma
PT   virus types.
XX
PS   Disclosure; Col 37-38; 96pp; English.
XX
CC   The invention relates to new oligonucleotide probes and primers used for
CC   the detection of human papillomaviruses (HPV) which are not genital types
CC   6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
CC   to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC   primers can be used to detect these HPV types in conjunction with the
CC   consensus primers and typing probes AAT44733-T44906, which are based on
CC   and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC   sequences. Detection of the amplification prods. is done with probes
CC   derived from consensus sequences found in all characterised HPV
CC   sequences. The negative strand primers AAT44821-6 are used with positive
CC   strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
CC   the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
CC   are detected using the E6 consensus probes AAT44839-40, specific for
CC   these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;

  Query Match             50.0%;  Score 5;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRCWW 6
              |||||
Db         15 RRCWW 11


RESULT 29
AAT77998
ID   AAT77998 standard; DNA; 20 BP.
XX
AC   AAT77998;
XX
DT   25-MAR-2003  (revised)
DT   06-OCT-1997  (first entry)
XX
DE   Human papillomavirus E6 negative strand consensus primer WD163.
XX
KW   Human; papillomavirus; HPV; primer; amplification; PCR;
KW   polymerase chain reaction; E6; negative strand; detection; ss.
XX
OS   Synthetic.
XX
PN   US5639871-A.
XX
PD   17-JUN-1997.
XX
PF   01-JUN-1995;   95US-00457648.
```

XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 29-AUG-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
XX
PA (HOFF) ROCHE MOLECULAR SYSTEMS INC.
XX
PI Impraim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;
PI Gravitt PE;
XX
DR WPI; 1997-332084/30.
XX
PT New oligo:nucleotide probes for human papilloma-virus - used for
PT detecting and typing HPV and for detecting previously unknown HPV types
PT and subtypes.
XX
PS Disclosure; Col 111-112; 94pp; English.
XX
CC The present sequence is a human papillomavirus (HPV) E6 negative strand
CC consensus primer. (Updated on 25-MAR-2003 to correct PF field.) (Updated
CC on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;

Query Match 50.0%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWGYY 9
||||||
Db 11 WWGYY 15

RESULT 30
AAT77998/c
ID AAT77998 standard; DNA; 20 BP.
XX
AC AAT77998;
XX
DT 25-MAR-2003 (revised)
DT 06-OCT-1997 (first entry)
XX
DE Human papillomavirus E6 negative strand consensus primer WD163.
XX
KW Human; papillomavirus; HPV; primer; amplification; PCR;
KW polymerase chain reaction; E6; negative strand; detection; ss.
XX
OS Synthetic.
XX
PN US5639871-A.
XX
PD 17-JUN-1997.
XX
PF 01-JUN-1995; 95US-00457648.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 29-AUG-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
XX
PA (HOFF) ROCHE MOLECULAR SYSTEMS INC.
XX
PI Impraim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;
PI Gravitt PE;
XX
DR WPI; 1997-332084/30.
XX
PT New oligo:nucleotide probes for human papilloma-virus - used for
PT detecting and typing HPV and for detecting previously unknown HPV types
PT and subtypes.
XX
PS Disclosure; Col 111-112; 94pp; English.
XX
CC The present sequence is a human papillomavirus (HPV) E6 negative strand
CC consensus primer. (Updated on 25-MAR-2003 to correct PF field.) (Updated
CC on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 20 BP; 3 A; 3 C; 5 G; 2 T; 0 U; 7 Other;

Query Match 50.0%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCWW 6
|||||
Db 15 RRCWW 11

RESULT 31
ABN87013
ID ABN87013 standard; RNA; 16 BP.
XX
AC ABN87013;
XX
DT 29-JUL-2002 (first entry)
XX
DE Histone mRNA stabilising sequence SEQ ID NO:51.
XX
KW Prodrug ribozyme; ribozyme; SV40; HCV; hepatitis C virus; target;
KW Simian virus 40; NS5B; viral infection; antiviral; cytostatic; HBV;
KW antiallergic; immunosuppressive; gene therapy; AIDS; hepatitis B virus;
KW cancer; leukaemia; genetic defect; allergy; autoimmune disease;
KW familial genetic disease; primary genetic disease; ss.
XX
OS Synthetic.
XX
PN WO200014252-A1.
XX
PD 16-MAR-2000.
XX
PF 02-SEP-1999; 99WO-JP004767.
XX
PR 03-SEP-1998; 98JP-00249900.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Tohdoh N, Yamamoto H, Sudo Y;
XX
DR WPI; 2000-256997/22.
XX
PT Novel ribozyme prodrug without RNA-cleaving activity, for use e.g. in
PT gene therapy to treat viral infections, cancers and diseases due to
PT defective genes.
XX
PS Disclosure; Page 96; 116pp; Japanese.
XX
CC The present invention describes a gene (I) encoding a ribozyme prodrug
CC comprising an intervening sequence removable by splicing, and/or lacking
CC RNA-cleaving activity. Also described are: (i) an expression vector
CC comprising (I) and preferably further comprising a tissue-specific
CC promoter; (ii) a ribozyme prodrug comprising an intervening sequence in
CC the ribozyme sequence removable by splicing, and lacking RNA-cleaving
CC activity; (iii) a drug composition comprising (I); and (iv) the in vivo
CC production of mature ribozyme with RNA-cleaving activity by introducing
CC (I) into a eukaryote. (I) has antiviral, cytostatic, antiallergic and
CC immunosuppressive activities, and can be used in ribozyme and gene
CC therapy. The ribozyme prodrug is useful e.g. in gene therapy,
CC particularly for treating viral infections such as AIDS and those due to
CC hepatitis B virus (HBV) and hepatitis C virus (HCV), cancers including
CC those of the liver, pancreas and colon, and leukaemia, and diseases
CC caused by genetic defects such as allergy, autoimmune diseases, familial

CC genetic diseases and primary genetic diseases. The ribozyme prodrug,
CC without RNA-cleaving activity, is encoded by a gene with an intervening
CC sequence in the ribozyme sequence which can be spliced off in cytoplasm
CC to give a functional ribozyme. The present sequence is used in the
CC exemplification of the present invention
XX
SQ Sequence 16 BP; 1 A; 2 C; 2 G; 0 T; 3 U; 8 Other;

Query Match 40.0%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
||||
Db 12 RRRC 15

RESULT 32
ABN87013/c
ID ABN87013 standard; RNA; 16 BP.
XX
AC ABN87013;
XX
DT 29-JUL-2002 (first entry)
XX
DE Histone mRNA stabilising sequence SEQ ID NO:51.
XX
KW Prodrug ribozyme; ribozyme; SV40; HCV; hepatitis C virus; target;
KW Simian virus 40; NS5B; viral infection; antiviral; cytostatic; HBV;
KW antiallergic; immunosuppressive; gene therapy; AIDS; hepatitis B virus;
KW cancer; leukaemia; genetic defect; allergy; autoimmune disease;
KW familial genetic disease; primary genetic disease; ss.
XX
OS Synthetic.
XX
PN WO200014252-A1.
XX
PD 16-MAR-2000.
XX
PF 02-SEP-1999; 99WO-JP004767.
XX
PR 03-SEP-1998; 98JP-00249900.
XX
PA (SUMU) SUMITOMO PHARM CO LTD.
XX
PI Tohdoh N, Yamamoto H, Sudo Y;
XX
DR WPI; 2000-256997/22.
XX
PT Novel ribozyme prodrug without RNA-cleaving activity, for use e.g. in
PT gene therapy to treat viral infections, cancers and diseases due to
PT defective genes.
XX
PS Disclosure; Page 96; 116pp; Japanese.
XX
CC The present invention describes a gene (I) encoding a ribozyme prodrug
CC comprising an intervening sequence removable by splicing, and/or lacking
CC RNA-cleaving activity. Also described are: (i) an expression vector
CC comprising (I) and preferably further comprising a tissue-specific
CC promoter; (ii) a ribozyme prodrug comprising an intervening sequence in
CC the ribozyme sequence removable by splicing, and lacking RNA-cleaving
CC activity; (iii) a drug composition comprising (I); and (iv) the in vivo
CC production of mature ribozyme with RNA-cleaving activity by introducing
CC (I) into a eukaryote. (I) has antiviral, cytostatic, antiallergic and
CC immunosuppressive activities, and can be used in ribozyme and gene
CC therapy. The ribozyme prodrug is useful e.g. in gene therapy,
CC particularly for treating viral infections such as AIDS and those due to
CC hepatitis B virus (HBV) and hepatitis C virus (HCV), cancers including
CC those of the liver, pancreas and colon, and leukaemia, and diseases
CC caused by genetic defects such as allergy, autoimmune diseases, familial
CC genetic diseases and primary genetic diseases. The ribozyme prodrug,
CC without RNA-cleaving activity, is encoded by a gene with an intervening
CC sequence in the ribozyme sequence which can be spliced off in cytoplasm
CC to give a functional ribozyme. The present sequence is used in the
CC exemplification of the present invention
XX
SQ Sequence 16 BP; 1 A; 2 C; 2 G; 0 T; 3 U; 8 Other;

Query Match 40.0%; Score 4; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
||||
Db 5 RRRC 2

RESULT 33
ABQ81373
ID ABQ81373 standard; DNA; 19 BP.
XX
AC ABQ81373;
XX
DT 12-DEC-2002 (first entry)
XX
DE Matrix metalloproteinase sense PCR primer.
XX
KW Mitogen activated protein kinase; MAPK; signal transduction;
KW matrix metalloproteinase; MMP; enzyme; human; invasion-associated gene;
KW cytostatic; glioma; cancer; therapy; assay; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200247535-A2.
XX
PD 20-JUN-2002.
XX
PF 14-DEC-2001; 2001WO-US047766.
XX
PR 14-DEC-2000; 2000US-0255548P.
XX
PA (NYXI-) NYXIS NEURO THERAPIES INC.
XX
PI Yamamoto H, Moskal J;
XX
DR WPI; 2002-713241/77.
XX
PT Identifying a modulator of mitogen-activated protein kinase pathway, by
PT contacting a cell transfected with recombinant construct encoding
PT reporter gene, with a compound and detecting change in reporter gene
PT expression.
XX
PS Example 1; Page 11; 36pp; English.
XX
CC The present sequence is that of a degenerate sense PCR primer for human
CC matrix metalloproteinase (MMP). Use with the antisense primer given in
CC ABQ81374 produces a PCR product of 400 bp. PCR was used to examine
CC expression of MMPs in a panel of human brain tumour cell lines. MMP-1 and
CC MMP-3 were expressed in SW-1088, U-87MG and U-118 glioma cell lines and
CC in SKN-SH neuroblastoma cells, while D54-MG glioma cells expressed low
CC levels of MMP-3 with no MMP-1 expression. Neither MMP-1 nor MMP-3 was
CC expressed in U-373 MG or SNB-19, and 3 other neuroblastoma cell lines
CC showed no MMP expression. MMP-10 expression was found in SW1088 and U-
CC 87MG glioma cell lines. No MMP-10 mRNA expression was found in
CC neuroblastoma cell lines. The invention provides a method of identifying
CC a compound affecting the mitogen-activated protein kinase (MAPK) pathway.
CC This involves contacting a test compound with a cell stably transfected
CC with a recombinant construct comprising a reporter gene operatively
CC linked to a c-fos promoter, and detecting a change in the expression of
CC the reporter gene. The cell constitutively expresses low levels of an
CC invasion-associated gene (e.g. MMP), whereby stimulation of the invasion-
CC associated gene occurs via activation of the MAPK pathway. Assay systems
CC are provided to identify compounds that modulate expression of MMP-1 and
CC MMP-3 in cancer cells. Such compounds are useful in cancer therapy
XX
SQ Sequence 19 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 4 Other;

```
  Query Match             40.0%;  Score 4;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WGYY 9
              ||||
Db          6 WGYY 9
```

RESULT 34
ABQ81373/c
ID ABQ81373 standard; DNA; 19 BP.
XX
AC ABQ81373;
XX
DT 12-DEC-2002 (first entry)
XX
DE Matrix metalloproteinase sense PCR primer.
XX
KW Mitogen activated protein kinase; MAPK; signal transduction;
KW matrix metalloproteinase; MMP; enzyme; human; invasion-associated gene;
KW cytostatic; glioma; cancer; therapy; assay; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200247535-A2.
XX
PD 20-JUN-2002.
XX
PF 14-DEC-2001; 2001WO-US047766.
XX
PR 14-DEC-2000; 2000US-0255548P.
XX
PA (NYXI-) NYXIS NEURO THERAPIES INC.
XX
PI Yamamoto H, Moskal J;
XX
DR WPI; 2002-713241/77.
XX
PT Identifying a modulator of mitogen-activated protein kinase pathway, by
PT contacting a cell transfected with recombinant construct encoding
PT reporter gene, with a compound and detecting change in reporter gene
PT expression.
XX
PS Example 1; Page 11; 36pp; English.
XX
CC The present sequence is that of a degenerate sense PCR primer for human
CC matrix metalloproteinase (MMP). Use with the antisense primer given in
CC ABQ81374 produces a PCR product of 400 bp. PCR was used to examine
CC expression of MMPs in a panel of human brain tumour cell lines. MMP-1 and
CC MMP-3 were expressed in SW-1088, U-87MG and U-118 glioma cell lines and
CC in SKN-SH neuroblastoma cells, while D54-MG glioma cells expressed low
CC levels of MMP-3 with no MMP-1 expression. Neither MMP-1 nor MMP-3 was
CC expressed in U-373 MG or SNB-19, and 3 other neuroblastoma cell lines
CC showed no MMP expression. MMP-10 expression was found in SW1088 and U-
CC 87MG glioma cell lines. No MMP-10 mRNA expression was found in
CC neuroblastoma cell lines. The invention provides a method of identifying
CC a compound affecting the mitogen-activated protein kinase (MAPK) pathway.
CC This involves contacting a test compound with a cell stably transfected
CC with a recombinant construct comprising a reporter gene operatively
CC linked to a c-fos promoter, and detecting a change in the expression of
CC the reporter gene. The cell constitutively expresses low levels of an
CC invasion-associated gene (e.g. MMP), whereby stimulation of the invasion-
CC associated gene occurs via activation of the MAPK pathway. Assay systems
CC are provided to identify compounds that modulate expression of MMP-1 and
CC MMP-3 in cancer cells. Such compounds are useful in cancer therapy
XX
SQ Sequence 19 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 4 Other;

```
  Query Match             40.0%;  Score 4;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRCW 5
              ||||
Db          9 RRCW 6
```

RESULT 35
AAD27333
ID AAD27333 standard; DNA; 19 BP.
XX
AC AAD27333;
XX
DT 18-APR-2002 (first entry)
XX
DE Human MMP cDNA cloning sense RT-PCR primer.
XX
KW Human; cancer; urokinase-type plasminogen activator; uPA; inflammation;
KW Ets-1 transcription factor; N-acetylglucosaminyltransferase V; GnT-V;
KW matrix-type metalloproteinase; MMP-1; MMP-3; gene therapy; c-ets-1;
KW reverse transcription PCR; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200196606-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US019248.
XX
PR 14-JUN-2000; 2000US-00593488.
XX
PA (NYXI-) NYXIS NEURO THERAPIES INC.
XX
PI Yamamoto H, Kroes R, Moskal JR;
XX
DR WPI; 2002-130746/17.
XX
PT Identifying a compound for treating cancer, comprises detecting
PT transcription factor Ets-1, N-acetylglucosaminyltransferase V, urokinase-
PT type plasminogen activator, matrix-type metalloproteinase-1 and -3 gene
PT expression.
XX
PS Example 1; Page 20; 63pp; English.
XX
CC The invention relates to a method of identifying a compound for treating
CC cancer. The method involves detecting the expression of a panel of
CC sequences selected from transcription factor Ets-1, urokinase-type
CC plasminogen activator (uPA), N-acetylglucosaminyltransferase V (GnT-V),
CC matrix-type metalloproteinase (MMP)-1 and MMP-3 in the cell. The method
CC is useful for identifying a compound that affects a cell, particularly a
CC cancer cell or glioma cell, or a cell that is involved in inflammation.
CC It is used for diagnosing and/or treating cancer or other conditions that
CC are affected by one or more members of a panel of genes or their protein
CC product. The method is also useful for drug discovery, drug safety
CC evaluations and in gene therapy. The present sequence is reverse
CC transcription PCR (RT-PCR) primer used to clone human MMP cDNA
XX
SQ Sequence 19 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 4 Other;

```
  Query Match             40.0%;  Score 4;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WGYY 9
              ||||
Db          6 WGYY 9
```

RESULT 36
AAD27333/c
ID AAD27333 standard; DNA; 19 BP.
XX
AC AAD27333;

XX
DT 18-APR-2002 (first entry)
XX
DE Human MMP cDNA cloning sense RT-PCR primer.
XX
KW Human; cancer; urokinase-type plasminogen activator; uPA; inflammation;
KW Ets-1 transcription factor; N-acetylglucosaminyltransferase V; GnT-V;
KW matrix-type metalloproteinase; MMP-1; MMP-3; gene therapy; c-ets-1;
KW reverse transcription PCR; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200196606-A2.
XX
PD 20-DEC-2001.
XX
PF 14-JUN-2001; 2001WO-US019248.
XX
PR 14-JUN-2000; 2000US-00593488.
XX
PA (NYXI-) NYXIS NEURO THERAPIES INC.
XX
PI Yamamoto H, Kroes R, Moskal JR;
XX
DR WPI; 2002-130746/17.
XX
PT Identifying a compound for treating cancer, comprises detecting
PT transcription factor Ets-1, N-acetylglucosaminyltransferase V, urokinase-
PT type plasminogen activator, matrix-type metalloproteinase-1 and -3 gene
PT expression.
XX
PS Example 1; Page 20; 63pp; English.
XX
CC The invention relates to a method of identifying a compound for treating
CC cancer. The method involves detecting the expression of a panel of
CC sequences selected from transcription factor Ets-1, urokinase-type
CC plasminogen activator (uPA), N-acetylglucosaminyltransferase V (GnT-V),
CC matrix-type metalloproteinase (MMP)-1 and MMP-3 in the cell. The method
CC is useful for identifying a compound that affects a cell, particularly a
CC cancer cell or glioma cell, or a cell that is involved in inflammation.
CC It is used for diagnosing and/or treating cancer or other conditions that
CC are affected by one or more members of a panel of genes or their protein
CC product. The method is also useful for drug discovery, drug safety
CC evaluations and in gene therapy. The present sequence is reverse
CC transcription PCR (RT-PCR) primer used to clone human MMP cDNA
XX
SQ Sequence 19 BP; 2 A; 5 C; 5 G; 3 T; 0 U; 4 Other;

Query Match 40.0%; Score 4; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5
||||
Db 9 RRCW 6

RESULT 37
AAQ56430
ID AAQ56430 standard; DNA; 20 BP.
XX
AC AAQ56430;
XX
DT 25-MAR-2003 (revised)
DT 29-JUL-1994 (first entry)
XX
DE E6 consensus negative strand primer WD164.
XX
KW Human papilloma virus; amplification; polymerase chain reaction; PCR;
KW detection; assay; genital; ss.
XX
OS Synthetic.
XX
PN US5283171-A.
XX
PD 01-FEB-1994.
XX
PF 15-FEB-1991; 91US-00651356.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 29-AUG-1989; 89WO-US003747.
XX
PA (UYRP) UNIV ROCHESTER.
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;
XX
DR WPI; 1994-048082/06.
XX
PT Detection of genital human papilloma virus - by PCR amplification using
PT defined consensus primer pairs.
XX
PS Disclosure; Page 9; 13pp; English.
XX
CC The sequence is that of the human papilloma virus (HPV) E6 consensus
CC negative strand primer WD164 which was used in the amplification by PCR
CC of HPV DNA. It may be used as part of a simple and rapid assay method for
CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGYY 9
||||
Db 12 WGYY 15

RESULT 38
AAQ56430/c
ID AAQ56430 standard; DNA; 20 BP.
XX
AC AAQ56430;
XX
DT 25-MAR-2003 (revised)
DT 29-JUL-1994 (first entry)
XX
DE E6 consensus negative strand primer WD164.
XX
KW Human papilloma virus; amplification; polymerase chain reaction; PCR;
KW detection; assay; genital; ss.
XX
OS Synthetic.
XX
PN US5283171-A.
XX
PD 01-FEB-1994.
XX
PF 15-FEB-1991; 91US-00651356.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 29-AUG-1989; 89WO-US003747.
XX
PA (UYRP) UNIV ROCHESTER.
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;
XX
DR WPI; 1994-048082/06.
XX
PT Detection of genital human papilloma virus - by PCR amplification using

PT defined consensus primer pairs.
XX
PS Disclosure; Page 9; 13pp; English.
XX
CC The sequence is that of the human papilloma virus (HPV) E6 consensus
CC negative strand primer WD164 which was used in the amplification by PCR
CC of HPV DNA. It may be used as part of a simple and rapid assay method for
CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5
||||
Db 15 RRCW 12

RESULT 39
AAQ56428
ID AAQ56428 standard; DNA; 20 BP.
XX
AC AAQ56428;
XX
DT 25-MAR-2003 (revised)
DT 29-JUL-1994 (first entry)
XX
DE E6 consensus negative strand primer WD155.
XX
KW Human papilloma virus; amplification; polymerase chain reaction; PCR;
KW detection; assay; genital; ss.
XX
OS Synthetic.
XX
PN US5283171-A.
XX
PD 01-FEB-1994.
XX
PF 15-FEB-1991; 91US-00651356.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 29-AUG-1989; 89WO-US003747.
XX
PA (UYRP) UNIV ROCHESTER.
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;
XX
DR WPI; 1994-048082/06.
XX
PT Detection of genital human papilloma virus - by PCR amplification using
PT defined consensus primer pairs.
XX
PS Disclosure; Page 9; 13pp; English.
XX
CC The sequence is that of the human papilloma virus (HPV) E6 consensus
CC negative strand primer WD155 which was used in the amplification by PCR
CC of HPV DNA. It may be used as part of a simple and rapid assay method for
CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWGY 8
||||
Db 11 WWGY 14

RESULT 40
AAQ56428/c
ID AAQ56428 standard; DNA; 20 BP.
XX
AC AAQ56428;
XX
DT 25-MAR-2003 (revised)
DT 29-JUL-1994 (first entry)
XX
DE E6 consensus negative strand primer WD155.
XX
KW Human papilloma virus; amplification; polymerase chain reaction; PCR;
KW detection; assay; genital; ss.
XX
OS Synthetic.
XX
PN US5283171-A.
XX
PD 01-FEB-1994.
XX
PF 15-FEB-1991; 91US-00651356.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 29-AUG-1989; 89WO-US003747.
XX
PA (UYRP) UNIV ROCHESTER.
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Wolinsky SM, Broker TR, Ting Y, Manos MM, Wright DK;
XX
DR WPI; 1994-048082/06.
XX
PT Detection of genital human papilloma virus - by PCR amplification using
PT defined consensus primer pairs.
XX
PS Disclosure; Page 9; 13pp; English.
XX
CC The sequence is that of the human papilloma virus (HPV) E6 consensus
CC negative strand primer WD155 which was used in the amplification by PCR
CC of HPV DNA. It may be used as part of a simple and rapid assay method for
CC detecting and typing HPV in biological samples. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RCWW 6
||||
Db 14 RCWW 11

RESULT 41
AAT44824
ID AAT44824 standard; DNA; 20 BP.
XX
AC AAT44824;
XX
DT 25-MAR-2003 (revised)
DT 31-JAN-1997 (first entry)
XX
DE HPV E6 region negative strand primer WD155.
XX
KW Probe; primer; PCR; polymerase chain reaction; amplification;
KW human papillomavirus; consensus; ss.
XX
OS Synthetic.

XX
PN US5527898-A.
XX
PD 18-JUN-1996.
XX
PF 07-JUN-1995; 95US-00474542.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 09-SEP-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
XX
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
XX
DR WPI; 1996-299903/30.
XX
PT Nucleic acid hybridisation probes - specific for selected human papilloma
PT virus types.
XX
PS Disclosure; Col 37-38; 96pp; English.
XX
CC The invention relates to new oligonucleotide probes and primers used for
CC the detection of human papillomaviruses (HPV) which are not genital types
CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC primers can be used to detect these HPV types in conjunction with the
CC consensus primers and typing probes AAT44733-T44906, which are based on
CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC sequences. Detection of the amplification prods. is done with probes
CC derived from consensus sequences found in all characterised HPV
CC sequences. The negative strand primers AAT44821-6 are used with positive
CC strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
CC the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
CC are detected using the E6 consensus probes AAT44839-40, specific for
CC these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWGY 8
||||
Db 11 WWGY 14

RESULT 42
AAT44824/c
ID AAT44824 standard; DNA; 20 BP.
XX
AC AAT44824;
XX
DT 25-MAR-2003 (revised)
DT 31-JAN-1997 (first entry)
XX
DE HPV E6 region negative strand primer WD155.
XX
KW Probe; primer; PCR; polymerase chain reaction; amplification;
KW human papillomavirus; consensus; ss.
XX
OS Synthetic.
XX
PN US5527898-A.
XX
PD 18-JUN-1996.
XX
PF 07-JUN-1995; 95US-00474542.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 09-SEP-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
XX
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
XX
DR WPI; 1996-299903/30.
XX
PT Nucleic acid hybridisation probes - specific for selected human papilloma
PT virus types.
XX
PS Disclosure; Col 37-38; 96pp; English.
XX
CC The invention relates to new oligonucleotide probes and primers used for
CC the detection of human papillomaviruses (HPV) which are not genital types
CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC primers can be used to detect these HPV types in conjunction with the
CC consensus primers and typing probes AAT44733-T44906, which are based on
CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC sequences. Detection of the amplification prods. is done with probes
CC derived from consensus sequences found in all characterised HPV
CC sequences. The negative strand primers AAT44821-6 are used with positive
CC strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
CC the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
CC are detected using the E6 consensus probes AAT44839-40, specific for
CC these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RCWW 6
||||
Db 14 RCWW 11

RESULT 43
AAT44826
ID AAT44826 standard; DNA; 20 BP.
XX
AC AAT44826;
XX
DT 25-MAR-2003 (revised)
DT 31-JAN-1997 (first entry)
XX
DE HPV E6 region negative strand primer WD164.
XX
KW Probe; primer; PCR; polymerase chain reaction; amplification;
KW human papillomavirus; consensus; ss.
XX
OS Synthetic.
XX
PN US5527898-A.
XX
PD 18-JUN-1996.
XX
PF 07-JUN-1995; 95US-00474542.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 09-SEP-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
XX

PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
XX
DR WPI; 1996-299903/30.
XX
PT Nucleic acid hybridisation probes - specific for selected human papilloma
PT virus types.
XX
PS Disclosure; Col 37-38; 96pp; English.
XX
CC The invention relates to new oligonucleotide probes and primers used for
CC the detection of human papillomaviruses (HPV) which are not genital types
CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC primers can be used to detect these HPV types in conjunction with the
CC consensus primers and typing probes AAT44733-T44906, which are based on
CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC sequences. Detection of the amplification prods. is done with probes
CC derived from consensus sequences found in all characterised HPV
CC sequences. The negative strand primers AAT44821-6 are used with positive
CC strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
CC the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
CC are detected using the E6 consensus probes AAT44839-40, specific for
CC these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGYY 9
||||
Db 12 WGYY 15

RESULT 44
AAT44826/c
ID AAT44826 standard; DNA; 20 BP.
XX
AC AAT44826;
XX
DT 25-MAR-2003 (revised)
DT 31-JAN-1997 (first entry)
XX
DE HPV E6 region negative strand primer WD164.
XX
KW Probe; primer; PCR; polymerase chain reaction; amplification;
KW human papillomavirus; consensus; ss.
XX
OS Synthetic.
XX
PN US5527898-A.
XX
PD 18-JUN-1996.
XX
PF 07-JUN-1995; 95US-00474542.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 09-SEP-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
XX
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Bauer HM, Resnick RM, Greer CE, Manos MM, Zhang TY, Gravitt PE;
XX
DR WPI; 1996-299903/30.
XX
PT Nucleic acid hybridisation probes - specific for selected human papilloma
PT virus types.
XX
PS Disclosure; Col 37-38; 96pp; English.
XX
CC The invention relates to new oligonucleotide probes and primers used for
CC the detection of human papillomaviruses (HPV) which are not genital types
CC 6, 11, 16, 18 or 33. The probes and primers AAT44608-T44693 are esp. used
CC to detect HPV types 26, 31, 31B, 35, 39, 40, 43, 45, 51-59 and 68. The
CC primers can be used to detect these HPV types in conjunction with the
CC consensus primers and typing probes AAT44733-T44906, which are based on
CC and amplify fragments of the L1, E6, E7 and E1 regions of the HPV
CC sequences. Detection of the amplification prods. is done with probes
CC derived from consensus sequences found in all characterised HPV
CC sequences. The negative strand primers AAT44821-6 are used with positive
CC strand primers (AAT44813-6) to amplify short fragments of 225-250 bp from
CC the E6 region of HPV types 6, 11, 16, 18 and 33. The amplified fragments
CC are detected using the E6 consensus probes AAT44839-40, specific for
CC these short fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5
||||
Db 15 RRCW 12

RESULT 45
AAT77997
ID AAT77997 standard; DNA; 20 BP.
XX
AC AAT77997;
XX
DT 25-MAR-2003 (revised)
DT 06-OCT-1997 (first entry)
XX
DE Human papillomavirus E6 negative strand consensus primer WD155.
XX
KW Human; papillomavirus; HPV; primer; amplification; PCR;
KW polymerase chain reaction; E6; negative strand; detection; ss.
XX
OS Synthetic.
XX
PN US5639871-A.
XX
PD 17-JUN-1997.
XX
PF 01-JUN-1995; 95US-00457648.
XX
PR 09-SEP-1988; 88US-00243486.
PR 10-MAR-1989; 89US-00322550.
PR 29-AUG-1989; 89WO-US003747.
PR 14-NOV-1990; 90US-00613142.
PR 20-APR-1993; 93US-00050743.
PR 24-SEP-1993; 93US-00126452.
XX
PA (HOFF) ROCHE MOLECULAR SYSTEMS INC.
XX
PI Impraim CC, Manos MM, Bauer HM, Zhang TY, Greer CE, Resnick RM;
PI Gravitt PE;
XX
DR WPI; 1997-332084/30.
XX
PT New oligo:nucleotide probes for human papilloma-virus - used for
PT detecting and typing HPV and for detecting previously unknown HPV types
PT and subtypes.
XX
PS Disclosure; Col 111-112; 94pp; English.
XX
CC The present sequence is a human papillomavirus (HPV) E6 negative strand

```
CC   consensus primer. (Updated on 25-MAR-2003 to correct PF field.) (Updated
CC   on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;

  Query Match             40.0%;  Score 4;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWGY 8
              ||||
Db         11 WWGY 14


RESULT 46
AAT77997/c
ID   AAT77997 standard; DNA; 20 BP.
XX
AC   AAT77997;
XX
DT   25-MAR-2003  (revised)
DT   06-OCT-1997  (first entry)
XX
DE   Human papillomavirus E6 negative strand consensus primer WD155.
XX
KW   Human; papillomavirus; HPV; primer; amplification; PCR;
KW   polymerase chain reaction; E6; negative strand; detection; ss.
XX
OS   Synthetic.
XX
PN   US5639871-A.
XX
PD   17-JUN-1997.
XX
PF   01-JUN-1995;   95US-00457648.
XX
PR   09-SEP-1988;   88US-00243486.
PR   10-MAR-1989;   89US-00322550.
PR   29-AUG-1989;   89WO-US003747.
PR   14-NOV-1990;   90US-00613142.
PR   20-APR-1993;   93US-00050743.
PR   24-SEP-1993;   93US-00126452.
XX
PA   (HOFF ) ROCHE MOLECULAR SYSTEMS INC.
XX
PI   Impraim CC,  Manos MM,  Bauer HM,  Zhang TY,  Greer CE,  Resnick RM;
PI   Gravitt PE;
XX
DR   WPI; 1997-332084/30.
XX
PT   New oligo:nucleotide probes for human papilloma-virus - used for
PT   detecting and typing HPV and for detecting previously unknown HPV types
PT   and subtypes.
XX
PS   Disclosure; Col 111-112; 94pp; English.
XX
CC   The present sequence is a human papillomavirus (HPV) E6 negative strand
CC   consensus primer. (Updated on 25-MAR-2003 to correct PF field.) (Updated
CC   on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 20 BP; 2 A; 4 C; 4 G; 2 T; 0 U; 8 Other;

  Query Match             40.0%;  Score 4;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RCWW 6
              ||||
Db         14 RCWW 11


RESULT 47
AAT77999
ID   AAT77999 standard; DNA; 20 BP.
XX
AC   AAT77999;
XX
DT   25-MAR-2003  (revised)
DT   06-OCT-1997  (first entry)
XX
DE   Human papillomavirus E6 negative strand consensus primer WD164.
XX
KW   Human; papillomavirus; HPV; primer; amplification; PCR;
KW   polymerase chain reaction; E6; negative strand; detection; ss.
XX
OS   Synthetic.
XX
PN   US5639871-A.
XX
PD   17-JUN-1997.
XX
PF   01-JUN-1995;   95US-00457648.
XX
PR   09-SEP-1988;   88US-00243486.
PR   10-MAR-1989;   89US-00322550.
PR   29-AUG-1989;   89WO-US003747.
PR   14-NOV-1990;   90US-00613142.
PR   20-APR-1993;   93US-00050743.
PR   24-SEP-1993;   93US-00126452.
XX
PA   (HOFF ) ROCHE MOLECULAR SYSTEMS INC.
XX
PI   Impraim CC,  Manos MM,  Bauer HM,  Zhang TY,  Greer CE,  Resnick RM;
PI   Gravitt PE;
XX
DR   WPI; 1997-332084/30.
XX
PT   New oligo:nucleotide probes for human papilloma-virus - used for
PT   detecting and typing HPV and for detecting previously unknown HPV types
PT   and subtypes.
XX
PS   Disclosure; Col 111-112; 94pp; English.
XX
CC   The present sequence is a human papillomavirus (HPV) E6 negative strand
CC   consensus primer. (Updated on 25-MAR-2003 to correct PF field.) (Updated
CC   on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;

  Query Match             40.0%;  Score 4;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WGYY 9
              ||||
Db         12 WGYY 15


RESULT 48
AAT77999/c
ID   AAT77999 standard; DNA; 20 BP.
XX
AC   AAT77999;
XX
DT   25-MAR-2003  (revised)
DT   06-OCT-1997  (first entry)
XX
DE   Human papillomavirus E6 negative strand consensus primer WD164.
XX
KW   Human; papillomavirus; HPV; primer; amplification; PCR;
KW   polymerase chain reaction; E6; negative strand; detection; ss.
XX
OS   Synthetic.
XX
PN   US5639871-A.
XX
```

```
PD   17-JUN-1997.
XX
PF   01-JUN-1995;   95US-00457648.
XX
PR   09-SEP-1988;   88US-00243486.
PR   10-MAR-1989;   89US-00322550.
PR   29-AUG-1989;   89WO-US003747.
PR   14-NOV-1990;   90US-00613142.
PR   20-APR-1993;   93US-00050743.
PR   24-SEP-1993;   93US-00126452.
XX
PA   (HOFF ) ROCHE MOLECULAR SYSTEMS INC.
XX
PI   Impraim CC,  Manos MM,  Bauer HM,  Zhang TY,  Greer CE,  Resnick RM;
PI   Gravitt PE;
XX
DR   WPI; 1997-332084/30.
XX
PT   New oligo:nucleotide probes for human papilloma-virus - used for
PT   detecting and typing HPV and for detecting previously unknown HPV types
PT   and subtypes.
XX
PS   Disclosure; Col 111-112; 94pp; English.
XX
CC   The present sequence is a human papillomavirus (HPV) E6 negative strand
CC   consensus primer. (Updated on 25-MAR-2003 to correct PF field.) (Updated
CC   on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 20 BP; 2 A; 3 C; 4 G; 2 T; 0 U; 9 Other;

  Query Match             40.0%;  Score 4;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRCW 5
              ||||
Db         15 RRCW 12


RESULT 49
AAV10231
ID   AAV10231 standard; DNA; 20 BP.
XX
AC   AAV10231;
XX
DT   29-MAY-1998  (first entry)
XX
DE   p53 binding DNA consensus sequence.
XX
KW   Tumour suppressor; reporter molecule; detection; p53; identification;
KW   radiation therapy; biopsy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9745556-A1.
XX
PD   04-DEC-1997.
XX
PF   09-MAY-1997;   97WO-US006545.
XX
PR   31-MAY-1996;   96US-00657828.
XX
PA   (ONYX-) ONYX PHARM INC.
XX
PI   Fattaey A;
XX
DR   WPI; 1998-041761/04.
XX
PT   Determining tumour suppressor status of tumour - via transformation with
PT   construct expressing reporter gene if tumour suppressor is present.
XX
PS   Example 1; Page 19; 42pp; English.
XX
CC   This sequence represents a p53 DNA binding site consensus sequence which
CC   is used in an example of a novel method for determining the tumour
CC   suppressor status of a tumour. The method involves administering, to the
CC   tumour, a novel construct comprising a nucleic acid molecule encoding a
CC   reporter molecule and a nucleic acid molecule capable of binding the
CC   tumour suppressor, so that binding causes the reporter molecule to be
CC   expressed, and determining if the reporter molecule is produced in the
CC   tumour. In this example the tumour suppressor is p53, and the method can
CC   be used to identify tumours, particularly of the head and neck, suitable
CC   for radiation therapy. This method is rapid and can be performed in vivo,
CC   eliminating the need for biopsy samples or cell lysis
XX
SQ   Sequence 20 BP; 2 A; 2 C; 2 G; 2 T; 0 U; 12 Other;

  Query Match             40.0%;  Score 4;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db          1 RRRC 4


RESULT 50
AAV10231/c
ID   AAV10231 standard; DNA; 20 BP.
XX
AC   AAV10231;
XX
DT   29-MAY-1998  (first entry)
XX
DE   p53 binding DNA consensus sequence.
XX
KW   Tumour suppressor; reporter molecule; detection; p53; identification;
KW   radiation therapy; biopsy; ss.
XX
OS   Homo sapiens.
XX
PN   WO9745556-A1.
XX
PD   04-DEC-1997.
XX
PF   09-MAY-1997;   97WO-US006545.
XX
PR   31-MAY-1996;   96US-00657828.
XX
PA   (ONYX-) ONYX PHARM INC.
XX
PI   Fattaey A;
XX
DR   WPI; 1998-041761/04.
XX
PT   Determining tumour suppressor status of tumour - via transformation with
PT   construct expressing reporter gene if tumour suppressor is present.
XX
PS   Example 1; Page 19; 42pp; English.
XX
CC   This sequence represents a p53 DNA binding site consensus sequence which
CC   is used in an example of a novel method for determining the tumour
CC   suppressor status of a tumour. The method involves administering, to the
CC   tumour, a novel construct comprising a nucleic acid molecule encoding a
CC   reporter molecule and a nucleic acid molecule capable of binding the
CC   tumour suppressor, so that binding causes the reporter molecule to be
CC   expressed, and determining if the reporter molecule is produced in the
CC   tumour. In this example the tumour suppressor is p53, and the method can
CC   be used to identify tumours, particularly of the head and neck, suitable
CC   for radiation therapy. This method is rapid and can be performed in vivo,
CC   eliminating the need for biopsy samples or cell lysis
XX
SQ   Sequence 20 BP; 2 A; 2 C; 2 G; 2 T; 0 U; 12 Other;

  Query Match             40.0%;  Score 4;  DB 2;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
```

```
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         20 RRRC 17


RESULT 51
ADF44299
ID   ADF44299 standard; DNA; 20 BP.
XX
AC   ADF44299;
XX
DT   12-FEB-2004  (first entry)
XX
DE   HPV PCR primer E1350L.
XX
KW   detection; human papillomavirus; HPV subtype; PCR; primer; ss.
XX
OS   Human papillomavirus.
XX
PN   JP2002360271-A.
XX
PD   17-DEC-2002.
XX
PF   28-NOV-2001; 2001JP-00362595.
XX
PR   04-MAY-2001; 2001TW-00110785.
XX
PA   (KING-) KING CAR FOOD IND CO LTD.
XX
DR   WPI; 2003-600935/57.
XX
PT   A detecting apparatus and a detecting method for identifying the subtypes
PT   of many species of human papilloma viruses at the same time and a
PT   composition for the detection.
XX
PS   Example 2.3.1; SEQ ID NO 656; 166pp; Japanese.
XX
CC   This invention describes a novel detecting apparatus for identifying the
CC   subtypes of human papillomaviruses (HPV) contained in a sample which
CC   comprises a carrier which can load sample, a first oligonucleotide loaded
CC   on first part of the carrier and a second oligonucleotide loaded on
CC   second part of carrier, in which first and second oligonucleotides
CC   hybridise with the DNA of the first and the second HPV subtype and can
CC   identify HPV subtype contained in sample at the same time. This sequence
CC   represents a PCR primer used in the method of the invention.
XX
SQ   Sequence 20 BP; 6 A; 1 C; 3 G; 3 T; 0 U; 7 Other;

  Query Match             40.0%;  Score 4;  DB 10;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db          6 GYYY 9


RESULT 52
ADF44299/c
ID   ADF44299 standard; DNA; 20 BP.
XX
AC   ADF44299;
XX
DT   12-FEB-2004  (first entry)
XX
DE   HPV PCR primer E1350L.
XX
KW   detection; human papillomavirus; HPV subtype; PCR; primer; ss.
XX
OS   Human papillomavirus.
XX
PN   JP2002360271-A.
XX
PD   17-DEC-2002.
XX
PF   28-NOV-2001; 2001JP-00362595.
XX
PR   04-MAY-2001; 2001TW-00110785.
XX
PA   (KING-) KING CAR FOOD IND CO LTD.
XX
DR   WPI; 2003-600935/57.
XX
PT   A detecting apparatus and a detecting method for identifying the subtypes
PT   of many species of human papilloma viruses at the same time and a
PT   composition for the detection.
XX
PS   Example 2.3.1; SEQ ID NO 656; 166pp; Japanese.
XX
CC   This invention describes a novel detecting apparatus for identifying the
CC   subtypes of human papillomaviruses (HPV) contained in a sample which
CC   comprises a carrier which can load sample, a first oligonucleotide loaded
CC   on first part of the carrier and a second oligonucleotide loaded on
CC   second part of carrier, in which first and second oligonucleotides
CC   hybridise with the DNA of the first and the second HPV subtype and can
CC   identify HPV subtype contained in sample at the same time. This sequence
CC   represents a PCR primer used in the method of the invention.
XX
SQ   Sequence 20 BP; 6 A; 1 C; 3 G; 3 T; 0 U; 7 Other;

  Query Match             40.0%;  Score 4;  DB 10;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db          9 RRRC 6


RESULT 53
AAH44952
ID   AAH44952 standard; DNA; 21 BP.
XX
AC   AAH44952;
XX
DT   11-SEP-2003  (revised)
DT   05-SEP-2001  (first entry)
XX
DE   HIV Gp41 region specific probe H-E-M&O-1696P.
XX
KW   Multiple viral agent detection; human immunodeficiency virus; HIV;
KW   Hepatitis C virus; HCV; Hepatitis B virus; Hepatitis C virus; HCV;
KW   blood transfusion; blood donation; viral infection; probe; ss.
XX
OS   Human immunodeficiency virus 1.
XX
PN   WO200136442-A1.
XX
PD   25-MAY-2001.
XX
PF   17-NOV-2000; 2000WO-US031738.
XX
PR   17-NOV-1999;   99US-0165916P.
XX
PA   (JIJJ/) JI J.
PA   (MANA/) MANAK M.
PA   (WUKK/) WU K.
PA   (CHEN/) CHEN X.
PA   (YANG/) YANG L.
XX
PI   Ji J,  Manak M,  Wu K,  Chen X,  Yang L;
XX
DR   WPI; 2001-355605/37.
XX
```

PT Simultaneous detection of HIV, HBV and HCV in samples useful to test
PT donated blood for viral infection comprises amplification of nucleic
PT acids.
XX
PS Disclosure; Page 14; 51pp; English.
XX
CC This invention relates to a method for detecting multiple viral agents in
CC a sample. The method consists of amplifying nucleic acids from Human
CC immunodeficiency virus (HIV), Hepatitis C virus (HCV), and or Hepatitis B
CC virus (HBV) using a mixture of primers specific for HBV, HCV HIV-1 type M
CC and HIV-1 type O and detecting their presence. Included in the invention
CC is a kit for the detection of HIV, HCV, HBV and combinations of them in a
CC blood or blood product sample. The method can be used to test blood
CC donated for transfusions for the presence of infection with HIV, HBV or
CC HCV. The present sequence represents a probe specific for the gp41 region
CC of HIV, which can be used in the method of the invention. (Updated on 11-
CC SEP-2003 to standardise OS field)
XX
SQ Sequence 21 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 4 Other;

Query Match 40.0%; Score 4; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5
||||
Db 11 RRCW 14

RESULT 54
AAH44952/c
ID AAH44952 standard; DNA; 21 BP.
XX
AC AAH44952;
XX
DT 11-SEP-2003 (revised)
DT 05-SEP-2001 (first entry)
XX
DE HIV Gp41 region specific probe H-E-M&O-1696P.
XX
KW Multiple viral agent detection; human immunodeficiency virus; HIV;
KW Hepatitis C virus; HCV; Hepatitis B virus; Hepatitis C virus; HCV;
KW blood transfusion; blood donation; viral infection; probe; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200136442-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031738.
XX
PR 17-NOV-1999; 99US-0165916P.
XX
PA (JIJJ/) JI J.
PA (MANA/) MANAK M.
PA (WUKK/) WU K.
PA (CHEN/) CHEN X.
PA (YANG/) YANG L.
XX
PI Ji J, Manak M, Wu K, Chen X, Yang L;
XX
DR WPI; 2001-355605/37.
XX
PT Simultaneous detection of HIV, HBV and HCV in samples useful to test
PT donated blood for viral infection comprises amplification of nucleic
PT acids.
XX
PS Disclosure; Page 14; 51pp; English.
XX
CC This invention relates to a method for detecting multiple viral agents in
CC a sample. The method consists of amplifying nucleic acids from Human
CC immunodeficiency virus (HIV), Hepatitis C virus (HCV), and or Hepatitis B
CC virus (HBV) using a mixture of primers specific for HBV, HCV HIV-1 type M
CC and HIV-1 type O and detecting their presence. Included in the invention
CC is a kit for the detection of HIV, HCV, HBV and combinations of them in a
CC blood or blood product sample. The method can be used to test blood
CC donated for transfusions for the presence of infection with HIV, HBV or
CC HCV. The present sequence represents a probe specific for the gp41 region
CC of HIV, which can be used in the method of the invention. (Updated on 11-
CC SEP-2003 to standardise OS field)
XX
SQ Sequence 21 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 4 Other;

Query Match 40.0%; Score 4; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGYY 9
||||
Db 14 WGYY 11

RESULT 55
ADA50047
ID ADA50047 standard; DNA; 25 BP.
XX
AC ADA50047;
XX
DT 20-NOV-2003 (first entry)
XX
DE Pig cDNA encoding cytotoxic T lymphocyte A4 degenerate PCR primer #1.
XX
KW Immunosuppressive; cellular immune response; humoral immune response;
KW cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation;
KW transplant rejection; ss; PCR; human; primer; rabbit; cow.
XX
OS Homo sapiens.
OS Oryctolagus cuniculus.
OS Bos taurus.
XX
PN US2003086940-A1.
XX
PD 08-MAY-2003.
XX
PF 20-AUG-2002; 2002US-00225519.
XX
PR 10-AUG-2001; 2001US-00928267.
XX
PA (COST/) COSTA C.
PA (PIZZ/) PIZZOLATO M.
PA (FODO/) FODOR W.
XX
PI Costa C, Pizzolato M, Fodor W;
XX
DR WPI; 2003-625623/59.
XX
PT New chimeric proteins comprising a first domain and a second domain
PT capable of inhibiting a cellular and humoral immune response,
PT respectively, useful for regulating humoral and cellular effector
PT functions of the immune system.
XX
PS Example 2; Page 9; 59pp; English.
XX
CC The invention relates to a chimaeric protein comprising a first domain
CC capable of inhibiting a cellular immune response and a second domain
CC capable of inhibiting a humoral immune response. Also included are a
CC chimaeric DNA construct (comprising a DNA sequence encoding a domain
CC capable of inhibiting a cellular immune response and a DNA sequence
CC encoding a domain capable of inhibiting a humoral immune response), a
CC cloning vector comprising the DNA construct, a host cell transformed by
CC the vector, a transgenic cell, tissue, organ or mammal comprising the
CC chimaeric protein, producing a mammal, mammalian organ, tissue or cells,
CC where the mammal is useful as an organ donor for a human or organ, tissue
CC or cells transplant into a human, by inserting a nucleic acid encoding a
CC chimaeric protein defined above into the mammal, organ, tissue or cells,

CC where the protein is expressed in the mammal, organ, tissue or cells,
CC defined regions of the DNA appearing as ADA50036 which encodes the pig
CC CTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined
CC regions of the CTLA4 protein ADA50037. The chimaeric protein is useful in
CC the protection of the porcine cell after xenotransplantation into a
CC human, and in inhibiting humoral and cellular defence mechanism.
CC Chimaeras were produced comprising pig CTLA4 (cellular immune response
CC region) and human CD59 (humoral response region), and of CTLA4 and human
CC DAF (not defined). The present sequence is a degenerate PCR primer used
CC to isolate the cDNA encoding pig CTLA4.
XX
SQ Sequence 25 BP; 2 A; 6 C; 6 G; 2 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
||||
Db 19 GYYY 22

RESULT 56
ADA50047/c
ID ADA50047 standard; DNA; 25 BP.
XX
AC ADA50047;
XX
DT 20-NOV-2003 (first entry)
XX
DE Pig cDNA encoding cytotoxic T lymphocyte A4 degenerate PCR primer #1.
XX
KW Immunosuppressive; cellular immune response; humoral immune response;
KW cytotoxic T lymphocyte A4; CD152; CTLA4; CD59; xenotransplantation;
KW transplant rejection; ss; PCR; human; primer; rabbit; cow.
XX
OS Homo sapiens.
OS Oryctolagus cuniculus.
OS Bos taurus.
XX
PN US2003086940-A1.
XX
PD 08-MAY-2003.
XX
PF 20-AUG-2002; 2002US-00225519.
XX
PR 10-AUG-2001; 2001US-00928267.
XX
PA (COST/) COSTA C.
PA (PIZZ/) PIZZOLATO M.
PA (FODO/) FODOR W.
XX
PI Costa C, Pizzolato M, Fodor W;
XX
DR WPI; 2003-625623/59.
XX
PT New chimeric proteins comprising a first domain and a second domain
PT capable of inhibiting a cellular and humoral immune response,
PT respectively, useful for regulating humoral and cellular effector
PT functions of the immune system.
XX
PS Example 2; Page 9; 59pp; English.
XX
CC The invention relates to a chimaeric protein comprising a first domain
CC capable of inhibiting a cellular immune response and a second domain
CC capable of inhibiting a humoral immune response. Also included are a
CC chimaeric DNA construct (comprising a DNA sequence encoding a domain
CC capable of inhibiting a cellular immune response and a DNA sequence
CC encoding a domain capable of inhibiting a humoral immune response), a
CC cloning vector comprising the DNA construct, a host cell transformed by
CC the vector, a transgenic cell, tissue, organ or mammal comprising the
CC chimaeric protein, producing a mammal, mammalian organ, tissue or cells,
CC where the mammal is useful as an organ donor for a human or organ, tissue
CC or cells transplant into a human, by inserting a nucleic acid encoding a
CC chimaeric protein defined above into the mammal, organ, tissue or cells,
CC where the protein is expressed in the mammal, organ, tissue or cells,
CC defined regions of the DNA appearing as ADA50036 which encodes the pig
CC CTLA4 (cytotoxic T lymphocyte A4, also known as CD152) and defined
CC regions of the CTLA4 protein ADA50037. The chimaeric protein is useful in
CC the protection of the porcine cell after xenotransplantation into a
CC human, and in inhibiting humoral and cellular defence mechanism.
CC Chimaeras were produced comprising pig CTLA4 (cellular immune response
CC region) and human CD59 (humoral response region), and of CTLA4 and human
CC DAF (not defined). The present sequence is a degenerate PCR primer used
CC to isolate the cDNA encoding pig CTLA4.
XX
SQ Sequence 25 BP; 2 A; 6 C; 6 G; 2 T; 0 U; 9 Other;

Query Match 40.0%; Score 4; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
||||
Db 22 RRRC 19

RESULT 57
AAZ57335
ID AAZ57335 standard; DNA; 26 BP.
XX
AC AAZ57335;
XX
DT 03-APR-2000 (first entry)
XX
DE TRH-producing microbe detection oligonucleotide probe.
XX
KW Thermostable direct haemolysin; TDH; TDH-related haemolysin; TRH;
KW Vibrio parahaemolyticus; detection; probe; ss.
XX
OS Vibrio parahaemolyticus.
XX
PN JP11318480-A.
XX
PD 24-NOV-1999.
XX
PF 15-MAY-1990; 99JP-00106870.
XX
PR 15-MAY-1990; 90JP-00124612.
XX
PA (TOYM) TOYOBO KK.
XX
DR WPI; 2000-100773/09.
XX
PT An oligonucleotide for the detection of Vibrio parahaemolyticus -
PT provides highly specific detection.
XX
PS Claim 1; Page 2; 6pp; Japanese.
XX
CC The present sequence represents an oligonucleotide which can be used for
CC the detection of a TRH-producing microbe (where TRH is a TDH-related
CC haemolysin, and TDH is thermostable direct haemolysin). The
CC oligonucleotide is useful for detection of Vibrio parahaemolyticus. The
CC oligonucleotide provides highly specific detection
XX
SQ Sequence 26 BP; 7 A; 7 C; 4 G; 0 T; 0 U; 8 Other;

Query Match 40.0%; Score 4; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
||||
Db 6 RRRC 9

```
RESULT 58
AAZ57335/c
ID   AAZ57335 standard; DNA; 26 BP.
XX
AC   AAZ57335;
XX
DT   03-APR-2000  (first entry)
XX
DE   TRH-producing microbe detection oligonucleotide probe.
XX
KW   Thermostable direct haemolysin; TDH; TDH-related haemolysin; TRH;
KW   Vibrio parahaemolyticus; detection; probe; ss.
XX
OS   Vibrio parahaemolyticus.
XX
PN   JP11318480-A.
XX
PD   24-NOV-1999.
XX
PF   15-MAY-1990;   99JP-00106870.
XX
PR   15-MAY-1990;   90JP-00124612.
XX
PA   (TOYM ) TOYOBO KK.
XX
DR   WPI; 2000-100773/09.
XX
PT   An oligonucleotide for the detection of Vibrio parahaemolyticus -
PT   provides highly specific detection.
XX
PS   Claim 1; Page 2; 6pp; Japanese.
XX
CC   The present sequence represents an oligonucleotide which can be used for
CC   the detection of a TRH-producing microbe (where TRH is a TDH-related
CC   haemolysin, and TDH is thermostable direct haemolysin). The
CC   oligonucleotide is useful for detection of Vibrio parahaemolyticus. The
CC   oligonucleotide provides highly specific detection
XX
SQ   Sequence 26 BP; 7 A; 7 C; 4 G; 0 T; 0 U; 8 Other;

  Query Match             40.0%;  Score 4;  DB 3;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db          9 GYYY 6


RESULT 59
AAQ24776
ID   AAQ24776 standard; DNA; 27 BP.
XX
AC   AAQ24776;
XX
DT   25-MAR-2003  (revised)
DT   10-NOV-1992  (first entry)
XX
DE   Arbitrary PCR primer #7.
XX
KW   abitrarily primed polymerase chain reaction; fingerprint; identification;
KW   restriction fragment length polymorphisms; RFLP; ss.
XX
OS   Synthetic.
XX
PN   WO9207095-A1.
XX
PD   30-APR-1992.
XX
PF   15-OCT-1991;   91WO-US007713.
XX
PR   15-OCT-1990;   90US-00598913.
PR   21-DEC-1990;   90US-00633095.
XX
PA   (STRA-) STRATAGENE.
XX
PI   Mcclelland M,  Welsh JT,  Sorge JA;
XX
DR   WPI; 1992-167173/20.
XX
PT   Arbitrarily primed polymerase chain reaction method - allows distinction
PT   of bacterial, mammalian and plant species due to individual specific
PT   fingerprints produced.
XX
PS   Claim 5; Page 55; 75pp; English.
XX
CC   This sequence is the pUC sequencing primer, which is being claimed as an
CC   "arbitrary PCR primer" for use in an arbitrarily primed PCR reaction (AP-
CC   PCR). The use of a single primer at low stringency conditions forms
CC   primed nucleic acids with a substantial degree of mismatching having
CC   occured between primer and target. Several rounds of PCR are then
CC   performed, reproducibly generating specific discrete products that can be
CC   resolved into a manageable number of individual bands providing a
CC   "fingerprint" of the template DNA. Used against genomic DNA from
CC   microorganisms, this method will generate a fingerprint of the organism
CC   concerned, thus giving a rapid and simple method of identification and
CC   classification. Only a small amount of biological material is required,
CC   and prior knowledge of the nucleotide sequence, molecular biology, or
CC   biochemistry of the organism is not necessary. Only one primer is
CC   required for amplification/identification. The method may also be used to
CC   generate detectable polymorphisms for genetic mapping of animals and
CC   humans. See also AAQ24770-7 (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

  Query Match             40.0%;  Score 4;  DB 2;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         15 RRRC 18


RESULT 60
AAQ24776/c
ID   AAQ24776 standard; DNA; 27 BP.
XX
AC   AAQ24776;
XX
DT   25-MAR-2003  (revised)
DT   10-NOV-1992  (first entry)
XX
DE   Arbitrary PCR primer #7.
XX
KW   abitrarily primed polymerase chain reaction; fingerprint; identification;
KW   restriction fragment length polymorphisms; RFLP; ss.
XX
OS   Synthetic.
XX
PN   WO9207095-A1.
XX
PD   30-APR-1992.
XX
PF   15-OCT-1991;   91WO-US007713.
XX
PR   15-OCT-1990;   90US-00598913.
PR   21-DEC-1990;   90US-00633095.
XX
PA   (STRA-) STRATAGENE.
XX
PI   Mcclelland M,  Welsh JT,  Sorge JA;
XX
DR   WPI; 1992-167173/20.
XX
PT   Arbitrarily primed polymerase chain reaction method - allows distinction
```

PT of bacterial, mammalian and plant species due to individual specific
PT fingerprints produced.
XX
PS Claim 5; Page 55; 75pp; English.
XX
CC This sequence is the pUC sequencing primer, which is being claimed as an
CC "arbitrary PCR primer" for use in an arbitrarily primed PCR reaction (AP-
CC PCR). The use of a single primer at low stringency conditions forms
CC primed nucleic acids with a substantial degree of mismatching having
CC occured between primer and target. Several rounds of PCR are then
CC performed, reproducibly generating specific discrete products that can be
CC resolved into a manageable number of individual bands providing a
CC "fingerprint" of the template DNA. Used against genomic DNA from
CC microorganisms, this method will generate a fingerprint of the organism
CC concerned, thus giving a rapid and simple method of identification and
CC classification. Only a small amount of biological material is required,
CC and prior knowledge of the nucleotide sequence, molecular biology, or
CC biochemistry of the organism is not necessary. Only one primer is
CC required for amplification/identification. The method may also be used to
CC generate detectable polymorphisms for genetic mapping of animals and
CC humans. See also AAQ24770-7 (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
||||
Db 18 GYYY 15

RESULT 61
AAT16364
ID AAT16364 standard; DNA; 27 BP.
XX
AC AAT16364;
XX
DT 25-MAR-2003 (revised)
DT 15-AUG-1996 (first entry)
XX
DE AP-PCR KpnR associated primer #2.
XX
KW Primer; arbitrarily primed polymerase chain reaction; AP-PCR;
KW amplification; identification; classification; bacteria; mammal; plant;
KW polymorphism; genetic mapping; eukaryote; ss.
XX
OS Synthetic.
XX
PN US5487985-A.
XX
PD 30-JAN-1996.
XX
PF 09-OCT-1992; 92US-00959119.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.
XX
PA (STRA-) STRATAGENE.
XX
PI Sorge JA, Mcclelland M, Welsh JT;
XX
DR WPI; 1996-105231/11.
XX
PT Novel arbitrarily primer polymerase chain reaction - produces a
PT fingerprint pattern of bands, useful for identification and
PT classification of organisms.
XX
PS Disclosure; Col 33; 31pp; English.
XX
CC The sequences given in AAT16358-64 are primers which were used to
CC demonstrate the method of the invention. The method of the invention is
CC termed "arbitrarily primed polymerase chain reaction" (AP-PCR) and causes
CC the generation of a set of discrete DNA sequences characteristic of a
CC genome. The method comprises forming a PCR admixt. by combining in a PCR
CC buffer, genomic DNA and at least one primer 10-50 bases in length and
CC then subjecting the admixt. to at least one PCR thermocycle. The
CC hybridisation step permits the arbitrary priming of the genomic DNA,
CC thereby producing a set of discrete DNA segments. The amplification
CC products are then contacted with a second primer, which matches the first
CC primer except that the second primer has one or more additional bases at
CC the 3' terminus, to form a second admixt. This second admixt. is then
CC subjected to PCR thermocycles in which the hybridisation does not permit
CC formation of primer-template duplexes with a substantial degree of
CC mismatch, thereby amplifying a discrete subset of DNA segments. The
CC method may be used for the identification and classification of organisms
CC such as bacteria, mammals and plants, and for the generation of
CC polymorphisms suitable for genetic mapping of eukaryotes. (Updated on 25-
CC MAR-2003 to correct PF field.)
XX
SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
||||
Db 15 RRRC 18

RESULT 62
AAT16364/c
ID AAT16364 standard; DNA; 27 BP.
XX
AC AAT16364;
XX
DT 25-MAR-2003 (revised)
DT 15-AUG-1996 (first entry)
XX
DE AP-PCR KpnR associated primer #2.
XX
KW Primer; arbitrarily primed polymerase chain reaction; AP-PCR;
KW amplification; identification; classification; bacteria; mammal; plant;
KW polymorphism; genetic mapping; eukaryote; ss.
XX
OS Synthetic.
XX
PN US5487985-A.
XX
PD 30-JAN-1996.
XX
PF 09-OCT-1992; 92US-00959119.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.
XX
PA (STRA-) STRATAGENE.
XX
PI Sorge JA, Mcclelland M, Welsh JT;
XX
DR WPI; 1996-105231/11.
XX
PT Novel arbitrarily primer polymerase chain reaction - produces a
PT fingerprint pattern of bands, useful for identification and
PT classification of organisms.
XX
PS Disclosure; Col 33; 31pp; English.
XX
CC The sequences given in AAT16358-64 are primers which were used to
CC demonstrate the method of the invention. The method of the invention is
CC termed "arbitrarily primed polymerase chain reaction" (AP-PCR) and causes
CC the generation of a set of discrete DNA sequences characteristic of a
CC genome. The method comprises forming a PCR admixt. by combining in a PCR
CC buffer, genomic DNA and at least one primer 10-50 bases in length and

CC then subjecting the admixt. to at least one PCR thermocycle. The
CC hybridisation step permits the arbitrary priming of the genomic DNA,
CC thereby producing a set of discrete DNA segments. The amplification
CC products are then contacted with a second primer, which matches the first
CC primer except that the second primer has one or more additional bases at
CC the 3' terminus, to form a second admixt. This second admixt. is then
CC subjected to PCR thermocycles in which the hybridisation does not permit
CC formation of primer-template duplexes with a substantial degree of
CC mismatch, thereby amplifying a discrete subset of DNA segments. The
CC method may be used for the identification and classification of organisms
CC such as bacteria, mammals and plants, and for the generation of
CC polymorphisms suitable for genetic mapping of eukaryotes. (Updated on 25-
CC MAR-2003 to correct PF field.)
XX
SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
||||
Db 18 GYYY 15

RESULT 63
AAZ40324
ID AAZ40324 standard; DNA; 27 BP.
XX
AC AAZ40324;
XX
DT 25-FEB-2000 (first entry)
XX
DE PCR primer TYKI-13 for tyrosine kinase coding sequence.
XX
KW PCR primer; tyrosine kinase; RAGE; human; gene expression analysis;
KW restriction analysis of gene expression; cancer; tumour tissue;
KW drug screening; cell biology; development; oncogenesis;
KW gene family member identification; marker gene identification; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9957324-A1.
XX
PD 11-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US009898.
XX
PR 06-MAY-1998; 98US-00073407.
XX
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Robinson DR, Kung H;
XX
DR WPI; 2000-052982/04.
XX
PT Restriction analysis of gene expression for characterizing expression in
PT different samples, identifying resistance markers, etc.,.
XX
PS Example 2; Page 37; 80pp; English.
XX
CC This sequence represents a PCR primer for restriction analysis of gene
CC expression (RAGE) for human tyrosine kinase coding sequence. The
CC invention relates to a method for the amplification of a sample using two
CC primers which are at least partially complementary to two conserved
CC regions, separated by a defined maximum and minimum distance in each gene
CC of a multigene family and isolation of the product of desired size range.
CC The method is used for analysing expressed genes in biological samples
CC especially two mRNA containing samples and thus different samples can be
CC compared (e.g. cancer and non-cancer samples) to identify differentially
CC expressed genes. RAGE on tyrosine kinase family in normal and tumour
CC tissue blocks showed elevated kinase (NYK and CSK) expression in tumour
CC samples compared to normal. The method also determines the effects of
CC factors like growth factors, cytokines, or hormones and drugs on the gene
CC expression and is also used in drug screening. The method can be utilised
CC for understanding many processes in normal cell biology, development and
CC oncogenesis. Many unidentified gene family members and the full length
CC gene corresponding to the sample can be identified and characterised. It
CC also provides means of identifying predictive marker genes for a given
CC condition. The method utilises smaller amounts of starting material than
CC non-PCR based technologies and it does not require the cloning and
CC sequencing of amplified products, thereby immediate, unambiguous signals
CC produced by known genes and unknown genes is identified. It is sensitive
CC (expression levels of genes transcripts which is 1 out of 2 million can
CC be identified). It is not labour-intensive, time-consuming and analyzes
CC specific gene families rather than all expressed genes. Parallel
CC processing of larger number of samples simultaneously is achieved and the
CC method can be utilised on multiple automated devices which measures the
CC expression levels of thousands of genes in hundreds of samples
XX
SQ Sequence 27 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 7 Other;

Query Match 40.0%; Score 4; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWGY 8
||||
Db 16 WWGY 19

RESULT 64
AAZ40324/c
ID AAZ40324 standard; DNA; 27 BP.
XX
AC AAZ40324;
XX
DT 25-FEB-2000 (first entry)
XX
DE PCR primer TYKI-13 for tyrosine kinase coding sequence.
XX
KW PCR primer; tyrosine kinase; RAGE; human; gene expression analysis;
KW restriction analysis of gene expression; cancer; tumour tissue;
KW drug screening; cell biology; development; oncogenesis;
KW gene family member identification; marker gene identification; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9957324-A1.
XX
PD 11-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US009898.
XX
PR 06-MAY-1998; 98US-00073407.
XX
PA (UYCA-) UNIV CASE WESTERN RESERVE.
XX
PI Robinson DR, Kung H;
XX
DR WPI; 2000-052982/04.
XX
PT Restriction analysis of gene expression for characterizing expression in
PT different samples, identifying resistance markers, etc.,.
XX
PS Example 2; Page 37; 80pp; English.
XX
CC This sequence represents a PCR primer for restriction analysis of gene
CC expression (RAGE) for human tyrosine kinase coding sequence. The
CC invention relates to a method for the amplification of a sample using two
CC primers which are at least partially complementary to two conserved
CC regions, separated by a defined maximum and minimum distance in each gene
CC of a multigene family and isolation of the product of desired size range.
CC The method is used for analysing expressed genes in biological samples

CC especially two mRNA containing samples and thus different samples can be
CC compared (e.g. cancer and non-cancer samples) to identify differentially
CC expressed genes. RAGE on tyrosine kinase family in normal and tumour
CC tissue blocks showed elevated kinase (NYK and CSK) expression in tumour
CC samples compared to normal. The method also determines the effects of
CC factors like growth factors, cytokines, or hormones and drugs on the gene
CC expression and is also used in drug screening. The method can be utilised
CC for understanding many processes in normal cell biology, development and
CC oncogenesis. Many unidentified gene family members and the full length
CC gene corresponding to the sample can be identified and characterised. It
CC also provides means of identifying predictive marker genes for a given
CC condition. The method utilises smaller amounts of starting material than
CC non-PCR based technologies and it does not require the cloning and
CC sequencing of amplified products, thereby immediate, unambiguous signals
CC produced by known genes and unknown genes is identified. It is sensitive
CC (expression levels of genes transcripts which is 1 out of 2 million can
CC be identified). It is not labour-intensive, time-consuming and analyzes
CC specific gene families rather than all expressed genes. Parallel
CC processing of larger number of samples simultaneously is achieved and the
CC method can be utilised on multiple automated devices which measures the
CC expression levels of thousands of genes in hundreds of samples
XX
SQ Sequence 27 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 7 Other;

Query Match 40.0%; Score 4; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RCWW 6
||||
Db 19 RCWW 16

RESULT 65
AAS04151
ID AAS04151 standard; DNA; 27 BP.
XX
AC AAS04151;
XX
DT 29-AUG-2001 (first entry)
XX
DE Degenerate pUC sequencing primer used in AP-PCR.
XX
KW AP-PCR; arbitrarily primed PCR; arbitrary primer; DNA fingerprint;
KW rapid organism identification; PCR primer; pUC; ss.
XX
OS Synthetic.
XX
PN US6207810-B1.
XX
PD 27-MAR-2001.
XX
PF 16-NOV-1993; 93US-00154364.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.
PR 09-OCT-1992; 92US-00959119.
XX
PA (STRA-) STRATAGENE.
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Mcclelland M, Welsh JT;
XX
DR WPI; 2001-298945/31.
XX
PT New isolated transforming growth factor-beta1 repressed transcript 1
PT polynucleotide useful for distinguishing growth-arrested cells from non-
PT growth-arrested cells, and for producing antibodies.
XX
PS Disclosure; Col 4; 48pp; English.
XX
CC The present sequence for degenerate pUC sequencing primer is used in AP-
CC PCR (arbitrarily primed PCR). Various arbitrary primers (AAS04145-
CC AAS04151, AAS04154-AAS04180) are described in the invention of a rapid
CC method for generating discrete DNA PCR products (characteristic of a
CC genome) as a "fingerprint". The AP-PCR method comprises priming the
CC target nucleic acid from a genome or cellular RNA preparation with a
CC single-stranded primer to form a primed nucleic acid with a substantial
CC degree of mismatch between the primer and target sequence. The primed
CC sequence is amplified by at least 1 cycle of PCR and the resulting
CC product amplified by a second step of PCR of at least 10 cycles. AP-PCR
CC is useful for the rapid identification of bacterial species and strains,
CC mammals and plants. AP-PCR is useful as it does not require knowledge of
CC the nucleotide sequence of the organism to be identified. Transforming
CC growth factor (TGF)-beta1 repressed transcript 1 (TRT1) polynucleotide
CC (AAS04153) which is associated with arrested cell growth is also
CC described. TRT1 is useful for the production of anti-sense RNA capable of
CC hybridising to the TRT1 polynucleotide, for producing antibodies, and for
CC distinguishing growth-arrested cells from non-growth-arrested cells. The
CC sequence for LF9.5m (AAU02482) which is associated with normal growth of
CC ovary cells is also given
XX
SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
||||
Db 15 RRRC 18

RESULT 66
AAS04151/c
ID AAS04151 standard; DNA; 27 BP.
XX
AC AAS04151;
XX
DT 29-AUG-2001 (first entry)
XX
DE Degenerate pUC sequencing primer used in AP-PCR.
XX
KW AP-PCR; arbitrarily primed PCR; arbitrary primer; DNA fingerprint;
KW rapid organism identification; PCR primer; pUC; ss.
XX
OS Synthetic.
XX
PN US6207810-B1.
XX
PD 27-MAR-2001.
XX
PF 16-NOV-1993; 93US-00154364.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.
PR 09-OCT-1992; 92US-00959119.
XX
PA (STRA-) STRATAGENE.
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Mcclelland M, Welsh JT;
XX
DR WPI; 2001-298945/31.
XX
PT New isolated transforming growth factor-beta1 repressed transcript 1
PT polynucleotide useful for distinguishing growth-arrested cells from non-
PT growth-arrested cells, and for producing antibodies.
XX
PS Disclosure; Col 4; 48pp; English.
XX
CC The present sequence for degenerate pUC sequencing primer is used in AP-
CC PCR (arbitrarily primed PCR). Various arbitrary primers (AAS04145-
CC AAS04151, AAS04154-AAS04180) are described in the invention of a rapid
CC method for generating discrete DNA PCR products (characteristic of a
CC genome) as a "fingerprint". The AP-PCR method comprises priming the

CC target nucleic acid from a genome or cellular RNA preparation with a
CC single-stranded primer to form a primed nucleic acid with a substantial
CC degree of mismatch between the primer and target sequence. The primed
CC sequence is amplified by at least 1 cycle of PCR and the resulting
CC product amplified by a second step of PCR of at least 10 cycles. AP-PCR
CC is useful for the rapid identification of bacterial species and strains,
CC mammals and plants. AP-PCR is useful as it does not require knowledge of
CC the nucleotide sequence of the organism to be identified. Transforming
CC growth factor (TGF)-beta1 repressed transcript 1 (TRT1) polynucleotide
CC (AAS04153) which is associated with arrested cell growth is also
CC described. TRT1 is useful for the production of anti-sense RNA capable of
CC hybridising to the TRT1 polynucleotide, for producing antibodies, and for
CC distinguishing growth-arrested cells from non-growth-arrested cells. The
CC sequence for LF9.5m (AAU02482) which is associated with normal growth of
CC ovary cells is also given
XX
SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
||||
Db 18 GYYY 15

RESULT 67
ADJ63790
ID ADJ63790 standard; DNA; 27 BP.
XX
AC ADJ63790;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer #2.
XX
KW ss; primer; identification; classification; polymorphism; tissue typing;
KW linkage map; restriction fragment length polymorphism; RFLP;
KW differential gene expression.
XX
OS Synthetic.
XX
PN US6696277-B1.
XX
PD 24-FEB-2004.
XX
PF 01-MAR-1995; 95US-00397335.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.
PR 09-OCT-1992; 92US-00959119.
XX
PA (STRA-) STRATAGENE.
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Mcclelland M, Welsh JT, Sorge JA;
XX
DR WPI; 2004-178457/17.
XX
PT Generating discrete set of DNA segments characteristic of sample of
PT single-stranded RNA, useful for identification and classification of
PT organisms, comprises carrying out arbitrarily primed polymerase chain
PT reaction.
XX
PS Disclosure; SEQ ID NO 8; 31pp; English.
XX
CC The invention relates to a method of generating a discrete set of DNA
CC characteristic of a single-stranded RNA sample. The method is useful for
CC generating a discrete set of DNA segments characteristic of a sample of
CC single-stranded RNA. The method is useful for identification and
CC classification of organisms, for the generation of polymorphisms suitable
CC for genetic mapping of eukaryotes, for the identification of tissue and
CC cell types, and for monitoring changes in the state of gene expression of
CC a cell or tissue. The method is used to verify the assignment of a
CC bacteria to a species. The method is useful in the generation of linkage
CC maps and can be correlated with restriction fragment length polymorphisms
CC (RFLPs) and other markers. The method is useful for generating detectable
CC polymorphisms, for use in genetic mapping of animals and humans. The
CC method is used to detect differential gene expression within tissues. The
CC method is useful for the identification of tissue as in tissue typing and
CC the identification of strain polymorphism and to detect changes in the
CC cell or tissue, e.g. particular genes respond to a particular agent or
CC treatment. The method will indicate a response to the treatment at the
CC level of differential gene expression. The method can identify species,
CC cell types or tissues rapidly. The method is capable of initiating
CC amplification in the presence of a substantial degree of mismatching. The
CC method requires only one primer sequence for amplification. The present
CC sequence represents a primer.
XX
SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
||||
Db 15 RRRC 18

RESULT 68
ADJ63790/c
ID ADJ63790 standard; DNA; 27 BP.
XX
AC ADJ63790;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer #2.
XX
KW ss; primer; identification; classification; polymorphism; tissue typing;
KW linkage map; restriction fragment length polymorphism; RFLP;
KW differential gene expression.
XX
OS Synthetic.
XX
PN US6696277-B1.
XX
PD 24-FEB-2004.
XX
PF 01-MAR-1995; 95US-00397335.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.
PR 09-OCT-1992; 92US-00959119.
XX
PA (STRA-) STRATAGENE.
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Mcclelland M, Welsh JT, Sorge JA;
XX
DR WPI; 2004-178457/17.
XX
PT Generating discrete set of DNA segments characteristic of sample of
PT single-stranded RNA, useful for identification and classification of
PT organisms, comprises carrying out arbitrarily primed polymerase chain
PT reaction.
XX
PS Disclosure; SEQ ID NO 8; 31pp; English.
XX
CC The invention relates to a method of generating a discrete set of DNA
CC characteristic of a single-stranded RNA sample. The method is useful for
CC generating a discrete set of DNA segments characteristic of a sample of
CC single-stranded RNA. The method is useful for identification and
CC classification of organisms, for the generation of polymorphisms suitable

CC for genetic mapping of eukaryotes, for the identification of tissue and
CC cell types, and for monitoring changes in the state of gene expression of
CC a cell or tissue. The method is used to verify the assignment of a
CC bacteria to a species. The method is useful in the generation of linkage
CC maps and can be correlated with restriction fragment length polymorphisms
CC (RFLPs) and other markers. The method is useful for generating detectable
CC polymorphisms, for use in genetic mapping of animals and humans. The
CC method is used to detect differential gene expression within tissues. The
CC method is useful for the identification of tissue as in tissue typing and
CC the identification of strain polymorphism and to detect changes in the
CC cell or tissue, e.g. particular genes respond to a particular agent or
CC treatment. The method will indicate a response to the treatment at the
CC level of differential gene expression. The method can identify species,
CC cell types or tissues rapidly. The method is capable of initiating
CC amplification in the presence of a substantial degree of mismatching. The
CC method requires only one primer sequence for amplification. The present
CC sequence represents a primer.
XX
SQ Sequence 27 BP; 4 A; 8 C; 7 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
||||
Db 18 GYYY 15

RESULT 69
ADJ63791
ID ADJ63791 standard; DNA; 27 BP.
XX
AC ADJ63791;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer for pUC sequencing.
XX
KW ss; primer; identification; classification; polymorphism; tissue typing;
KW linkage map; restriction fragment length polymorphism; RFLP;
KW differential gene expression.
XX
OS Synthetic.
XX
PN US6696277-B1.
XX
PD 24-FEB-2004.
XX
PF 01-MAR-1995; 95US-00397335.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.
PR 09-OCT-1992; 92US-00959119.
XX
PA (STRA-) STRATAGENE.
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Mcclelland M, Welsh JT, Sorge JA;
XX
DR WPI; 2004-178457/17.
XX
PT Generating discrete set of DNA segments characteristic of sample of
PT single-stranded RNA, useful for identification and classification of
PT organisms, comprises carrying out arbitrarily primed polymerase chain
PT reaction.
XX
PS Disclosure; SEQ ID NO 9; 31pp; English.
XX
CC The invention relates to a method of generating a discrete set of DNA
CC characteristic of a single-stranded RNA sample. The method is useful for
CC generating a discrete set of DNA segments characteristic of a sample of
CC single-stranded RNA. The method is useful for identification and
CC classification of organisms, for the generation of polymorphisms suitable
CC for genetic mapping of eukaryotes, for the identification of tissue and
CC cell types, and for monitoring changes in the state of gene expression of
CC a cell or tissue. The method is used to verify the assignment of a
CC bacteria to a species. The method is useful in the generation of linkage
CC maps and can be correlated with restriction fragment length polymorphisms
CC (RFLPs) and other markers. The method is useful for generating detectable
CC polymorphisms, for use in genetic mapping of animals and humans. The
CC method is used to detect differential gene expression within tissues. The
CC method is useful for the identification of tissue as in tissue typing and
CC the identification of strain polymorphism and to detect changes in the
CC cell or tissue, e.g. particular genes respond to a particular agent or
CC treatment. The method will indicate a response to the treatment at the
CC level of differential gene expression. The method can identify species,
CC cell types or tissues rapidly. The method is capable of initiating
CC amplification in the presence of a substantial degree of mismatching. The
CC method requires only one primer sequence for amplification. The present
CC sequence represents a pUC sequencing primer.
XX
SQ Sequence 27 BP; 4 A; 7 C; 8 G; 2 T; 0 U; 6 Other;

Query Match 40.0%; Score 4; DB 12; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
||||
Db 15 RRRC 18

RESULT 70
ADJ63791/c
ID ADJ63791 standard; DNA; 27 BP.
XX
AC ADJ63791;
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer for pUC sequencing.
XX
KW ss; primer; identification; classification; polymorphism; tissue typing;
KW linkage map; restriction fragment length polymorphism; RFLP;
KW differential gene expression.
XX
OS Synthetic.
XX
PN US6696277-B1.
XX
PD 24-FEB-2004.
XX
PF 01-MAR-1995; 95US-00397335.
XX
PR 15-OCT-1990; 90US-00598913.
PR 21-DEC-1990; 90US-00633095.
PR 09-OCT-1992; 92US-00959119.
XX
PA (STRA-) STRATAGENE.
PA (CALB-) CALIFORNIA INST BIOLOGICAL RES.
XX
PI Mcclelland M, Welsh JT, Sorge JA;
XX
DR WPI; 2004-178457/17.
XX
PT Generating discrete set of DNA segments characteristic of sample of
PT single-stranded RNA, useful for identification and classification of
PT organisms, comprises carrying out arbitrarily primed polymerase chain
PT reaction.
XX
PS Disclosure; SEQ ID NO 9; 31pp; English.
XX
CC The invention relates to a method of generating a discrete set of DNA
CC characteristic of a single-stranded RNA sample. The method is useful for
CC generating a discrete set of DNA segments characteristic of a sample of

```
CC   single-stranded RNA. The method is useful for identification and
CC   classification of organisms, for the generation of polymorphisms suitable
CC   for genetic mapping of eukaryotes, for the identification of tissue and
CC   cell types, and for monitoring changes in the state of gene expression of
CC   a cell or tissue. The method is used to verify the assignment of a
CC   bacteria to a species. The method is useful in the generation of linkage
CC   maps and can be correlated with restriction fragment length polymorphisms
CC   (RFLPs) and other markers. The method is useful for generating detectable
CC   polymorphisms, for use in genetic mapping of animals and humans. The
CC   method is used to detect differential gene expression within tissues. The
CC   method is useful for the identification of tissue as in tissue typing and
CC   the identification of strain polymorphism and to detect changes in the
CC   cell or tissue, e.g. particular genes respond to a particular agent or
CC   treatment. The method will indicate a response to the treatment at the
CC   level of differential gene expression. The method can identify species,
CC   cell types or tissues rapidly. The method is capable of initiating
CC   amplification in the presence of a substantial degree of mismatching. The
CC   method requires only one primer sequence for amplification. The present
CC   sequence represents a pUC sequencing primer.
XX
SQ   Sequence 27 BP; 4 A; 7 C; 8 G; 2 T; 0 U; 6 Other;

  Query Match             40.0%;  Score 4;  DB 12;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYYY 10
              ||||
Db         18 GYYY 15


RESULT 71
AAD46919
ID   AAD46919 standard; DNA; 30 BP.
XX
AC   AAD46919;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Histone 3' UTR DNA fragment #1.
XX
KW   Gene expression; transcript stability; drug screening; histone; ds.
XX
OS   Mammalia.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    4
FT                   /*tag=  a
FT                   /note= "This base can be repeated 20-40 times"
XX
PN   WO200272844-A1.
XX
PD   19-SEP-2002.
XX
PF   08-MAR-2002; 2002WO-AU000351.
XX
PR   09-MAR-2001; 2001US-0274770P.
XX
PA   (GENE-) GENE STREAM PTY LTD.
XX
PI   Daly J;
XX
DR   WPI; 2002-759847/82.
XX
PT   New expression vector useful for modulating gene expression, identifying
PT   and analyzing regulatory sequences, new targets and reagents for treating
PT   human diseases, comprises a transcribable polynucleotide encoding an RNA
PT   element.
XX
PS   Claim 11; Page 68; 103pp; English.
XX
CC   The present invention relates to novel expression vectors and/or reporter
CC   vectors providing kinetics of protein expression with improved temporal
CC   correlation to the promoter activity. The expression vectors comprise
CC   transcribable polynucleotides having sequences of nucleotides encoding
CC   RNA elements which modulates the stability of a transcript corresponding
CC   to the transcribable polynucleotide. The expression vectors are useful
CC   for modulating the stability of a transcript and determining expression
CC   of a polynucleotide of interest. They are useful for modulating gene
CC   expression, identifying and analysing regulatory sequences, new targets
CC   and reagents for treating human diseases and for drug screening. The
CC   present sequence is histone 3' untranslated region (UTR) DNA fragment.
CC   This sequence is used in the exemplification of the invention
XX
SQ   Sequence 30 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 9 Other;

  Query Match             40.0%;  Score 4;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         21 RRRC 24


RESULT 72
AAD46919/c
ID   AAD46919 standard; DNA; 30 BP.
XX
AC   AAD46919;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Histone 3' UTR DNA fragment #1.
XX
KW   Gene expression; transcript stability; drug screening; histone; ds.
XX
OS   Mammalia.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    4
FT                   /*tag=  a
FT                   /note= "This base can be repeated 20-40 times"
XX
PN   WO200272844-A1.
XX
PD   19-SEP-2002.
XX
PF   08-MAR-2002; 2002WO-AU000351.
XX
PR   09-MAR-2001; 2001US-0274770P.
XX
PA   (GENE-) GENE STREAM PTY LTD.
XX
PI   Daly J;
XX
DR   WPI; 2002-759847/82.
XX
PT   New expression vector useful for modulating gene expression, identifying
PT   and analyzing regulatory sequences, new targets and reagents for treating
PT   human diseases, comprises a transcribable polynucleotide encoding an RNA
PT   element.
XX
PS   Claim 11; Page 68; 103pp; English.
XX
CC   The present invention relates to novel expression vectors and/or reporter
CC   vectors providing kinetics of protein expression with improved temporal
CC   correlation to the promoter activity. The expression vectors comprise
CC   transcribable polynucleotides having sequences of nucleotides encoding
CC   RNA elements which modulates the stability of a transcript corresponding
CC   to the transcribable polynucleotide. The expression vectors are useful
CC   for modulating the stability of a transcript and determining expression
CC   of a polynucleotide of interest. They are useful for modulating gene
CC   expression, identifying and analysing regulatory sequences, new targets
CC   and reagents for treating human diseases and for drug screening. The
CC   present sequence is histone 3' untranslated region (UTR) DNA fragment.
```

```
CC   This sequence is used in the exemplification of the invention
XX
SQ   Sequence 30 BP; 7 A; 7 C; 3 G; 4 T; 0 U; 9 Other;

  Query Match             40.0%;  Score 4;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         14 RRRC 11


RESULT 73
AAD46937
ID   AAD46937 standard; DNA; 30 BP.
XX
AC   AAD46937;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Histone 3' UTR DNA fragment #2.
XX
KW   Gene expression; transcript stability; drug screening; histone;
KW   DNA-RNA hybrid; ds.
XX
OS   Mammalia.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    4
FT                   /*tag=  a
FT                   /note= "This base can be repeated 20-40 times"
FT   misc_RNA        15. .18
FT                   /*tag=  b
FT                   /label= RNA
XX
PN   WO200272844-A1.
XX
PD   19-SEP-2002.
XX
PF   08-MAR-2002; 2002WO-AU000351.
XX
PR   09-MAR-2001; 2001US-0274770P.
XX
PA   (GENE-) GENE STREAM PTY LTD.
XX
PI   Daly J;
XX
DR   WPI; 2002-759847/82.
XX
PT   New expression vector useful for modulating gene expression, identifying
PT   and analyzing regulatory sequences, new targets and reagents for treating
PT   human diseases, comprises a transcribable polynucleotide encoding an RNA
PT   element.
XX
PS   Example 15; Page 68; 103pp; English.
XX
CC   The present invention relates to novel expression vectors and/or reporter
CC   vectors providing kinetics of protein expression with improved temporal
CC   correlation to the promoter activity. The expression vectors comprise
CC   transcribable polynucleotides having sequences of nucleotides encoding
CC   RNA elements which modulates the stability of a transcript corresponding
CC   to the transcribable polynucleotide. The expression vectors are useful
CC   for modulating the stability of a transcript and determining expression
CC   of a polynucleotide of interest. They are useful for modulating gene
CC   expression, identifying and analysing regulatory sequences, new targets
CC   and reagents for treating human diseases and for drug screening. The
CC   present sequence is histone 3' untranslated region (UTR) DNA fragment.
CC   This sequence is used in the exemplification of the invention
XX
SQ   Sequence 30 BP; 7 A; 7 C; 3 G; 1 T; 3 U; 9 Other;

  Query Match             40.0%;  Score 4;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
Db         21 RRRC 24


RESULT 74
AAD46937/c
ID   AAD46937 standard; DNA; 30 BP.
XX
AC   AAD46937;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Histone 3' UTR DNA fragment #2.
XX
KW   Gene expression; transcript stability; drug screening; histone;
KW   DNA-RNA hybrid; ds.
XX
OS   Mammalia.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    4
FT                   /*tag=  a
FT                   /note= "This base can be repeated 20-40 times"
FT   misc_RNA        15. .18
FT                   /*tag=  b
FT                   /label= RNA
XX
PN   WO200272844-A1.
XX
PD   19-SEP-2002.
XX
PF   08-MAR-2002; 2002WO-AU000351.
XX
PR   09-MAR-2001; 2001US-0274770P.
XX
PA   (GENE-) GENE STREAM PTY LTD.
XX
PI   Daly J;
XX
DR   WPI; 2002-759847/82.
XX
PT   New expression vector useful for modulating gene expression, identifying
PT   and analyzing regulatory sequences, new targets and reagents for treating
PT   human diseases, comprises a transcribable polynucleotide encoding an RNA
PT   element.
XX
PS   Example 15; Page 68; 103pp; English.
XX
CC   The present invention relates to novel expression vectors and/or reporter
CC   vectors providing kinetics of protein expression with improved temporal
CC   correlation to the promoter activity. The expression vectors comprise
CC   transcribable polynucleotides having sequences of nucleotides encoding
CC   RNA elements which modulates the stability of a transcript corresponding
CC   to the transcribable polynucleotide. The expression vectors are useful
CC   for modulating the stability of a transcript and determining expression
CC   of a polynucleotide of interest. They are useful for modulating gene
CC   expression, identifying and analysing regulatory sequences, new targets
CC   and reagents for treating human diseases and for drug screening. The
CC   present sequence is histone 3' untranslated region (UTR) DNA fragment.
CC   This sequence is used in the exemplification of the invention
XX
SQ   Sequence 30 BP; 7 A; 7 C; 3 G; 1 T; 3 U; 9 Other;

  Query Match             40.0%;  Score 4;  DB 6;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRRC 4
              ||||
```

```
Db         14 RRRC 11


RESULT 75
AAQ30066
ID   AAQ30066 standard; DNA; 32 BP.
XX
AC   AAQ30066;
XX
DT   25-MAR-2003  (revised)
DT   04-APR-1993  (first entry)
XX
DE   Sequence of PCR primer VH Bam Back for the variable domain heavy chain
DE   (VH) of clone B.
XX
KW   Antibody; PCR primer; variable heavy chain; ss.
XX
OS   Synthetic.
XX
PN   WO9218534-A1.
XX
PD   29-OCT-1992.
XX
PF   23-APR-1992;   92WO-GB000746.
XX
PR   23-APR-1991;   91GB-00008652.
XX
PA   (ANTI-) ANTISOMA LTD.
XX
PI   Courtenay-Luck NS;
XX
DR   WPI; 1992-382045/46.
XX
PT   New peptide EPPT (Glu-Pro-Pro-Thr) - selectively binds mucin expressed by
PT   epithelial tumours, used for guiding toxins or labels to tumours
PT   expressing mucin.
XX
PS   Example; Table 1, Page 27; 50pp; English.
XX
CC   Clone B is a lymphoblastoid cell line (secreting antibody directed
CC   against a tumour-associated mucin mol.) derived from the EBV- transfoming
CC   and cloning of a patient's peripheral blood B-cells. After DNA isolation,
CC   the polymerase chain reaction (PCR) was employed, using oligonucleotide
CC   primers specific for the variable light and heavy chains of
CC   immunoglobulins (see AAQ30065, AAQ30066). (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 32 BP; 6 A; 6 C; 9 G; 5 T; 0 U; 6 Other;

  Query Match             40.0%;  Score 4;  DB 2;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db         28 CWWG 31


RESULT 76
AAQ30066/c
ID   AAQ30066 standard; DNA; 32 BP.
XX
AC   AAQ30066;
XX
DT   25-MAR-2003  (revised)
DT   04-APR-1993  (first entry)
XX
DE   Sequence of PCR primer VH Bam Back for the variable domain heavy chain
DE   (VH) of clone B.
XX
KW   Antibody; PCR primer; variable heavy chain; ss.
XX
OS   Synthetic.
XX
PN   WO9218534-A1.
XX
PD   29-OCT-1992.
XX
PF   23-APR-1992;   92WO-GB000746.
XX
PR   23-APR-1991;   91GB-00008652.
XX
PA   (ANTI-) ANTISOMA LTD.
XX
PI   Courtenay-Luck NS;
XX
DR   WPI; 1992-382045/46.
XX
PT   New peptide EPPT (Glu-Pro-Pro-Thr) - selectively binds mucin expressed by
PT   epithelial tumours, used for guiding toxins or labels to tumours
PT   expressing mucin.
XX
PS   Example; Table 1, Page 27; 50pp; English.
XX
CC   Clone B is a lymphoblastoid cell line (secreting antibody directed
CC   against a tumour-associated mucin mol.) derived from the EBV- transfoming
CC   and cloning of a patient's peripheral blood B-cells. After DNA isolation,
CC   the polymerase chain reaction (PCR) was employed, using oligonucleotide
CC   primers specific for the variable light and heavy chains of
CC   immunoglobulins (see AAQ30065, AAQ30066). (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 32 BP; 6 A; 6 C; 9 G; 5 T; 0 U; 6 Other;

  Query Match             40.0%;  Score 4;  DB 2;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWWG 7
              ||||
Db         31 CWWG 28


RESULT 77
AAV39802
ID   AAV39802 standard; cDNA; 38 BP.
XX
AC   AAV39802;
XX
DT   28-SEP-1998  (first entry)
XX
DE   Oligonucleotide SEQ ID NO:320 from WO9820166.
XX
KW   Mass spectrometry; diagnosis; detection; biological sample; infection;
KW   genetic disease; chromosomal abnormality; identification; heredity;
KW   pathogenic organism; telomerase activity; oncogene mutation;
KW   cancer-specific sequence; primer; ss.
XX
OS   Synthetic.
XX
PN   WO9820166-A2.
XX
PD   14-MAY-1998.
XX
PF   06-NOV-1997;   97WO-US020444.
XX
PR   06-NOV-1996;   96US-00744481.
PR   06-NOV-1996;   96US-00744590.
PR   06-NOV-1996;   96US-00746036.
PR   06-NOV-1996;   96US-00746055.
PR   23-JAN-1997;   97US-00786988.
PR   23-JAN-1997;   97US-00787639.
PR   19-SEP-1997;   97US-00933792.
PR   08-OCT-1997;   97US-00947801.
XX
PA   (SEQU-) SEQUENOM INC.
```

XX
PI Koster H, Tang K, Fu D, Siegert CW, Little DP, Higgins GS;
PI Braun A, Damhoffer-Demar B, Jurinke C, Van Den Boom D, Xiang G;
PI Lough DM;
XX
DR WPI; 1998-286975/25.
XX
PT Sequencing nucleic acid by mass spectrometric analysis - for detecting
PT nucleic acids, telomerase activity, oncogene mutations, or cancer-
PT specific sequences, for diagnosis of disease.
XX
PS Disclosure; Page 336; 478pp; English.
XX
CC A process has been developed for determining the sequence of a target
CC nucleic acid. The process comprises: (i) generating at least two
CC fragments (F) from the target nucleic acid; and (ii) analysing F by mass
CC spectrometry (MS). The sequences in AAV39483 to AAV39592 are specifically
CC claimed primers for use in the mass spectrometric analysis of the above
CC process. The process is used to detect genetic diseases (e.g.
CC haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's
CC disease, cystic fibrosis and many others) or chromosomal abnormalities
CC (or predisposition); infections and cancers; also for establishing
CC identity and heredity. Particular applications are diagnosis of
CC neuroblastoma, detecting telomerase, determining family relationships and
CC HLA compatibility, and in genetic fingerprinting. Compared with known
CC methods using MS, this process requires fewer specific reagents and is
CC better suited to automation. Extended primers are shorter; primer
CC annealing is more efficient and the process allows detection of many
CC sequences simultaneously. The present sequence represent an
CC oligonucleotide from the present invention, which is not actually
CC specified within the specification, only within the sequence listing
XX
SQ Sequence 38 BP; 10 A; 10 C; 7 G; 8 T; 0 U; 3 Other;

Query Match 40.0%; Score 4; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWWG 7
||||
Db 33 CWWG 36

RESULT 78
AAV39802/c
ID AAV39802 standard; cDNA; 38 BP.
XX
AC AAV39802;
XX
DT 28-SEP-1998 (first entry)
XX
DE Oligonucleotide SEQ ID NO:320 from WO9820166.
XX
KW Mass spectrometry; diagnosis; detection; biological sample; infection;
KW genetic disease; chromosomal abnormality; identification; heredity;
KW pathogenic organism; telomerase activity; oncogene mutation;
KW cancer-specific sequence; primer; ss.
XX
OS Synthetic.
XX
PN WO9820166-A2.
XX
PD 14-MAY-1998.
XX
PF 06-NOV-1997; 97WO-US020444.
XX
PR 06-NOV-1996; 96US-00744481.
PR 06-NOV-1996; 96US-00744590.
PR 06-NOV-1996; 96US-00746036.
PR 06-NOV-1996; 96US-00746055.
PR 23-JAN-1997; 97US-00786988.
PR 23-JAN-1997; 97US-00787639.
PR 19-SEP-1997; 97US-00933792.
PR 08-OCT-1997; 97US-00947801.
XX
PA (SEQU-) SEQUENOM INC.
XX
PI Koster H, Tang K, Fu D, Siegert CW, Little DP, Higgins GS;
PI Braun A, Damhoffer-Demar B, Jurinke C, Van Den Boom D, Xiang G;
PI Lough DM;
XX
DR WPI; 1998-286975/25.
XX
PT Sequencing nucleic acid by mass spectrometric analysis - for detecting
PT nucleic acids, telomerase activity, oncogene mutations, or cancer-
PT specific sequences, for diagnosis of disease.
XX
PS Disclosure; Page 336; 478pp; English.
XX
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CC process. The process is used to detect genetic diseases (e.g.
CC haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's
CC disease, cystic fibrosis and many others) or chromosomal abnormalities
CC (or predisposition); infections and cancers; also for establishing
CC identity and heredity. Particular applications are diagnosis of
CC neuroblastoma, detecting telomerase, determining family relationships and
CC HLA compatibility, and in genetic fingerprinting. Compared with known
CC methods using MS, this process requires fewer specific reagents and is
CC better suited to automation. Extended primers are shorter; primer
CC annealing is more efficient and the process allows detection of many
CC sequences simultaneously. The present sequence represent an
CC oligonucleotide from the present invention, which is not actually
CC specified within the specification, only within the sequence listing
XX
SQ Sequence 38 BP; 10 A; 10 C; 7 G; 8 T; 0 U; 3 Other;

Query Match 40.0%; Score 4; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWWG 7
||||
Db 36 CWWG 33

RESULT 79
AAA28440
ID AAA28440 standard; DNA; 6 BP.
XX
AC AAA28440;
XX
DT 29-AUG-2000 (first entry)
XX
DE Synthetic promoter conserved domain IIb.
XX
KW Artificial promoter; strong; weak; transgene expression; plant; ss.
XX
OS Synthetic.
XX
PN EP1002869-A1.
XX
PD 24-MAY-2000.
XX
PF 25-FEB-1999; 99EP-00301419.
XX
PR 09-NOV-1998; 98IN-DE003322.
XX
PA (COUL) CSIR COUNCIL SCI IND RES.
XX
PI Tuli R, Sawant SV, Singh PK, Gupta SK;
XX
DR WPI; 2000-341712/30.

XX
PT New chemically synthesized artificial promoter, useful high level
PT expression of transgenes in different organisms.
XX
PS Claim 6; Page 18; 40pp; English.
XX
CC A chemically synthesized promoter can comprise a conserved domain IIb as
CC shown here for high level expression of genes. Chemically synthesized
CC artificial promoters are new and comprise a DNA sequence designed for a
CC targeted level and pattern of gene expression by strategically putting
CC together several signature sequences identified by sequence alignment and
CC statistical analysis of a large database constructed for this purpose. A
CC method for chemically synthesizing an artificial promoter for expressing
CC genes at a desired level in different organisms is also claimed. The high
CC level expression in a plant using such an artificial promoter (e.g.
CC AAA28449) can be measured comprising polyethylene glycol (PEG) mediated
CC transformation of plant protoplasts as well as biolistic mediated
CC transformation of plant tissues including root, stem, intact leaf tissue
CC followed by transient GUS assay to compare with a natural CaMV 35S
CC promoter showing the desired level of activity. The promoter is useful
CC for high level expression of transgenes in different organisms and for
CC testing high level gene expression in plants (claimed). The promoter is
CC biologically active and is efficient and can be synthesized to express in
CC even the most complex organisms
XX
SQ Sequence 6 BP; 0 A; 2 C; 0 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
||||
Db 1 CWW 3

RESULT 80
AAA28440/c
ID AAA28440 standard; DNA; 6 BP.
XX
AC AAA28440;
XX
DT 29-AUG-2000 (first entry)
XX
DE Synthetic promoter conserved domain IIb.
XX
KW Artificial promoter; strong; weak; transgene expression; plant; ss.
XX
OS Synthetic.
XX
PN EP1002869-A1.
XX
PD 24-MAY-2000.
XX
PF 25-FEB-1999; 99EP-00301419.
XX
PR 09-NOV-1998; 98IN-DE003322.
XX
PA (COUL) CSIR COUNCIL SCI IND RES.
XX
PI Tuli R, Sawant SV, Singh PK, Gupta SK;
XX
DR WPI; 2000-341712/30.
XX
PT New chemically synthesized artificial promoter, useful high level
PT expression of transgenes in different organisms.
XX
PS Claim 6; Page 18; 40pp; English.
XX
CC A chemically synthesized promoter can comprise a conserved domain IIb as
CC shown here for high level expression of genes. Chemically synthesized
CC artificial promoters are new and comprise a DNA sequence designed for a
CC targeted level and pattern of gene expression by strategically putting
CC together several signature sequences identified by sequence alignment and
CC statistical analysis of a large database constructed for this purpose. A
CC method for chemically synthesizing an artificial promoter for expressing
CC genes at a desired level in different organisms is also claimed. The high
CC level expression in a plant using such an artificial promoter (e.g.
CC AAA28449) can be measured comprising polyethylene glycol (PEG) mediated
CC transformation of plant protoplasts as well as biolistic mediated
CC transformation of plant tissues including root, stem, intact leaf tissue
CC followed by transient GUS assay to compare with a natural CaMV 35S
CC promoter showing the desired level of activity. The promoter is useful
CC for high level expression of transgenes in different organisms and for
CC testing high level gene expression in plants (claimed). The promoter is
CC biologically active and is efficient and can be synthesized to express in
CC even the most complex organisms
XX
SQ Sequence 6 BP; 0 A; 2 C; 0 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7
|||
Db 6 WWG 4

RESULT 81
ADF42928
ID ADF42928 standard; DNA; 6 BP.
XX
AC ADF42928;
XX
DT 11-MAR-2004 (first entry)
XX
DE Methylated immunostimulatory oligonucleotide ODN #27 SEQ ID NO:27.
XX
KW lipid-methylated nucleic acid formulation; immune response;
KW lipid-nucleic acid; vaccine; immunostimulant; cytostatic;
KW antiinflammatory; antiarthritic; gene therapy; cancer; inflammation;
KW arthritis; immunodeficiency disorder;
KW methylated immunostimulatory oligonucleotide; ss.
XX
OS Synthetic.
XX
PN WO2003094963-A2.
XX
PD 20-NOV-2003.
XX
PF 12-MAY-2003; 2003WO-CA000678.
XX
PR 10-MAY-2002; 2002US-0379343P.
PR 07-NOV-2002; 2002US-00290545.
PR 04-APR-2003; 2003US-0460646P.
XX
PA (INEX-) INEX PHARM CORP.
XX
PI Tam YK, Semple S, Klimuk S, Chikh G;
XX
DR WPI; 2004-142698/14.
XX
PT Lipid-methylated nucleic acid formulation for stimulating an immune
PT response in an animal comprises a lipid component and a nucleic acid
PT component comprising a methylated nucleic acid sequence.
XX
PS Disclosure; SEQ ID NO 27; 102pp; English.
XX
CC The present invention describes a lipid-methylated nucleic acid
CC formulation for stimulating an immune response in an animal, comprising a
CC lipid component and a nucleic acid component which is a methylated
CC nucleic acid sequence. Also described: (1) an adjuvant comprising a lipid
CC -nucleic acid (LNA) formulation; (2) a vaccine comprising the LNA
CC formulation in combination with at least one target antigen; (3)
CC stimulating an enhanced host immune response to antigenic stimulation,

CC comprising administering to the host the LNA formulation; (4) stimulating
CC host dendritic cells in vivo, comprising contacting at least one
CC dendritic cell with the lipid-methylated nucleic acid formulation to a
CC host; and (5) simultaneously delivering antigenic and adjuvant immune
CC stimulation to antigen presenting cells, comprising the administration of
CC the LNA formulation associated with a target antigen. The lipid-
CC methylation nucleic acid formulation has immunostimulant, cytostatic,
CC antiinflammatory and antiarthritic activities, and can be used in
CC vaccines, and in gene therapy. The formulation and methods are useful in
CC stimulating a host's immune response to antigenic stimulation, or in
CC activating and/or expanding dendritic cell populations in response to
CC antigenic stimulation. They may be used for treating cancer,
CC inflammation, arthritis or immunodeficiency disorders. The present
CC sequence represents a methylated immunostimulatory oligonucleotide given
CC in the exemplification of the present invention.
XX
SQ Sequence 6 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 1 RRC 3

RESULT 82
ADF42928/c
ID ADF42928 standard; DNA; 6 BP.
XX
AC ADF42928;
XX
DT 11-MAR-2004 (first entry)
XX
DE Methylated immunostimulatory oligonucleotide ODN #27 SEQ ID NO:27.
XX
KW lipid-methylated nucleic acid formulation; immune response;
KW lipid-nucleic acid; vaccine; immunostimulant; cytostatic;
KW antiinflammatory; antiarthritic; gene therapy; cancer; inflammation;
KW arthritis; immunodeficiency disorder;
KW methylated immunostimulatory oligonucleotide; ss.
XX
OS Synthetic.
XX
PN WO2003094963-A2.
XX
PD 20-NOV-2003.
XX
PF 12-MAY-2003; 2003WO-CA000678.
XX
PR 10-MAY-2002; 2002US-0379343P.
PR 07-NOV-2002; 2002US-00290545.
PR 04-APR-2003; 2003US-0460646P.
XX
PA (INEX-) INEX PHARM CORP.
XX
PI Tam YK, Semple S, Klimuk S, Chikh G;
XX
DR WPI; 2004-142698/14.
XX
PT Lipid-methylated nucleic acid formulation for stimulating an immune
PT response in an animal comprises a lipid component and a nucleic acid
PT component comprising a methylated nucleic acid sequence.
XX
PS Disclosure; SEQ ID NO 27; 102pp; English.
XX
CC The present invention describes a lipid-methylated nucleic acid
CC formulation for stimulating an immune response in an animal, comprising a
CC lipid component and a nucleic acid component which is a methylated
CC nucleic acid sequence. Also described: (1) an adjuvant comprising a lipid
CC -nucleic acid (LNA) formulation; (2) a vaccine comprising the LNA
CC formulation in combination with at least one target antigen; (3)
CC stimulating an enhanced host immune response to antigenic stimulation,
CC comprising administering to the host the LNA formulation; (4) stimulating
CC host dendritic cells in vivo, comprising contacting at least one
CC dendritic cell with the lipid-methylated nucleic acid formulation to a
CC host; and (5) simultaneously delivering antigenic and adjuvant immune
CC stimulation to antigen presenting cells, comprising the administration of
CC the LNA formulation associated with a target antigen. The lipid-
CC methylation nucleic acid formulation has immunostimulant, cytostatic,
CC antiinflammatory and antiarthritic activities, and can be used in
CC vaccines, and in gene therapy. The formulation and methods are useful in
CC stimulating a host's immune response to antigenic stimulation, or in
CC activating and/or expanding dendritic cell populations in response to
CC antigenic stimulation. They may be used for treating cancer,
CC inflammation, arthritis or immunodeficiency disorders. The present
CC sequence represents a methylated immunostimulatory oligonucleotide given
CC in the exemplification of the present invention.
XX
SQ Sequence 6 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 6 RRC 4

RESULT 83
ADL35954
ID ADL35954 standard; DNA; 6 BP.
XX
AC ADL35954;
XX
DT 20-MAY-2004 (first entry)
XX
DE Non-methylated CpG motif consensus sequence.
XX
KW cosmetic; pharmaceutical; epithelial tissue; fabric softener;
KW hand washing product; body care product; hair care product; hair dye;
KW manual dishwashing product; nonmethylated CpG; antiinflammatory;
KW dermatological; antipsoriatic; endocrine; vulnerary; immunosuppressive;
KW interleukin-6 release inhibitor; interleukin-8 release inhibitor;
KW epithelial inflammation; inflammation-induced aging; psoriasis;
KW atopic eczema; dry skin; alopecia arreata; vitiligo; bullous disease;
KW graft versus host; UV-induced skin inflammation; parodontosis; ds.
XX
OS Unidentified.
XX
PN DE10233994-A1.
XX
PD 12-FEB-2004.
XX
PF 25-JUL-2002; 2002DE-01033994.
XX
PR 25-JUL-2002; 2002DE-01033994.
XX
PA (PHEN-) PHENION GMBH & CO KG.
XX
DR WPI; 2004-192562/19.
XX
PT Cosmetic or pharmaceutical composition for treatment of epithelial
PT tissue, especially to combat inflammation, comprises nucleic acids with
PT nonmethylated CpG units.
XX
PS Claim 8; Page 13; 19pp; German.
XX
CC This invention describes a novel cosmetic or pharmaceutical composition
CC for treatment of epithelial tissue comprising nucleic acids with
CC nonmethylated CpG units. The invention also describes a fabric softener,
CC hand washing product, body or hair care product, hair dye or manual
CC dishwashing product comprising nucleic acids with nonmethylated CpG
CC units. The nucleic acids are 6-10 nucleotides in length and include the

CC sequence 5'-A/GA/GCGC/TC/T-3'. The nucleic acids are optionally modified
CC by replacing phosphodiester linkages with methyl phosphonate,
CC phosphoramidate, phosphorothioate or hydroxylamine linkages, by replacing
CC ribose with other hexo- or pentopyranoses with 3',5'-carbocyclically
CC bridged 2'-deoxyribose derivatives or by replacing sugar phosphate units
CC with carboxamide units based on amino acid derivatives, e.g. N-(2-
CC aminoethyl)glycine. The nucleic acids are packed into liposomes. The
CC products of the invention have antiinflammatory, dermatological,
CC antipsoriatic, general endocrine, vulnerary and immunosuppressive
CC activity and act as interleukin-6 or interleukin-8 release inhibitors.
CC The composition is especially useful for preventing or treating
CC epithelial inflammations, including inflammation-induced aging,
CC psoriasis, atopic eczema, dry skin, alopecia arreata, vitiligo, bullous
CC diseases, graft versus host reactions, UV-induced skin inflammation and
CC parodontosis.
XX
SQ Sequence 6 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 1 RRC 3

RESULT 84
ADL35954/c
ID ADL35954 standard; DNA; 6 BP.
XX
AC ADL35954;
XX
DT 20-MAY-2004 (first entry)
XX
DE Non-methylated CpG motif consensus sequence.
XX
KW cosmetic; pharmaceutical; epithelial tissue; fabric softener;
KW hand washing product; body care product; hair care product; hair dye;
KW manual dishwashing product; nonmethylated CpG; antiinflammatory;
KW dermatological; antipsoriatic; endocrine; vulnerary; immunosuppressive;
KW interleukin-6 release inhibitor; interleukin-8 release inhibitor;
KW epithelial inflammation; inflammation-induced aging; psoriasis;
KW atopic eczema; dry skin; alopecia arreata; vitiligo; bullous disease;
KW graft versus host; UV-induced skin inflammation; parodontosis; ds.
XX
OS Unidentified.
XX
PN DE10233994-A1.
XX
PD 12-FEB-2004.
XX
PF 25-JUL-2002; 2002DE-01033994.
XX
PR 25-JUL-2002; 2002DE-01033994.
XX
PA (PHEN-) PHENION GMBH & CO KG.
XX
DR WPI; 2004-192562/19.
XX
PT Cosmetic or pharmaceutical composition for treatment of epithelial
PT tissue, especially to combat inflammation, comprises nucleic acids with
PT nonmethylated CpG units.
XX
PS Claim 8; Page 13; 19pp; German.
XX
CC This invention describes a novel cosmetic or pharmaceutical composition
CC for treatment of epithelial tissue comprising nucleic acids with
CC nonmethylated CpG units. The invention also describes a fabric softener,
CC hand washing product, body or hair care product, hair dye or manual
CC dishwashing product comprising nucleic acids with nonmethylated CpG
CC units. The nucleic acids are 6-10 nucleotides in length and include the
CC sequence 5'-A/GA/GCGC/TC/T-3'. The nucleic acids are optionally modified
CC by replacing phosphodiester linkages with methyl phosphonate,
CC phosphoramidate, phosphorothioate or hydroxylamine linkages, by replacing
CC ribose with other hexo- or pentopyranoses with 3',5'-carbocyclically
CC bridged 2'-deoxyribose derivatives or by replacing sugar phosphate units
CC with carboxamide units based on amino acid derivatives, e.g. N-(2-
CC aminoethyl)glycine. The nucleic acids are packed into liposomes. The
CC products of the invention have antiinflammatory, dermatological,
CC antipsoriatic, general endocrine, vulnerary and immunosuppressive
CC activity and act as interleukin-6 or interleukin-8 release inhibitors.
CC The composition is especially useful for preventing or treating
CC epithelial inflammations, including inflammation-induced aging,
CC psoriasis, atopic eczema, dry skin, alopecia arreata, vitiligo, bullous
CC diseases, graft versus host reactions, UV-induced skin inflammation and
CC parodontosis.
XX
SQ Sequence 6 BP; 0 A; 1 C; 1 G; 0 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 6 RRC 4

RESULT 85
AAZ88744
ID AAZ88744 standard; DNA; 7 BP.
XX
AC AAZ88744;
XX
DT 16-MAY-2000 (first entry)
XX
DE V. cholera VCR element inverse core DNA sequence.
XX
KW Diversity-selected gene; restriction enzyme; adhesin; toxin;
KW detoxifying enzyme; VCR element; ss.
XX
OS Vibrio cholerae.
XX
PN WO9964632-A1.
XX
PD 16-DEC-1999.
XX
PF 11-JUN-1999; 99WO-US013295.
XX
PR 12-JUN-1998; 98US-0089086P.
PR 12-JUN-1998; 98US-0089101P.
XX
PA (NEWE) NEW ENGLAND BIOLABS INC.
XX
PI Raleigh EA, Vaisvila R, Morgan RD;
XX
DR WPI; 2000-116558/10.
XX
PT Cloning intact genes used to isolate genes for restriction enzymes.
XX
PS Disclosure; Page 5; 97pp; English.
XX
CC This invention describes a novel method for cloning intact, diversity-
CC selected genes (I) from within gene cassettes (GC) which comprises
CC identifying DNA repeats that flank GC, hybridizing oligonucleotides (ON)
CC to these repeats and amplification to produce DNA fragments containing
CC (I), ligating these fragments into a vector and transforming cells with
CC the vector. This method is used to clone a wide variety of prokaryotic
CC genes that provide a selective advantage under particular conditions,
CC particularly those that encode restriction enzymes (used as reagents in
CC molecular biology); adhesins (for use in coating or for targeting
CC molecules or organisms to particular sites, e.g. for competitive
CC exclusion of a selected pathogen); detoxifying enzymes; toxins that
CC interact with a host, e.g. for synthesis of inhibitors or antagonists of
CC the toxin, or in vaccination, or a modification methyltransferase. Intact

```
CC   genes can be cloned directly with a high probability that the orientation
CC   of expression is known in advance and low probability of association with
CC   extraneous, possibly toxic, genes. This sequence represents a VCR element
CC   inverse core DNA sequence isolated from Vibrio cholera
XX
SQ   Sequence 7 BP; 2 A; 1 C; 0 G; 0 T; 0 U; 4 Other;

  Query Match             30.0%;  Score 3;  DB 3;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          2 YYY 4


RESULT 86
AAZ88744/c
ID   AAZ88744 standard; DNA; 7 BP.
XX
AC   AAZ88744;
XX
DT   16-MAY-2000  (first entry)
XX
DE   V. cholera VCR element inverse core DNA sequence.
XX
KW   Diversity-selected gene; restriction enzyme; adhesin; toxin;
KW   detoxifying enzyme; VCR element; ss.
XX
OS   Vibrio cholerae.
XX
PN   WO9964632-A1.
XX
PD   16-DEC-1999.
XX
PF   11-JUN-1999;   99WO-US013295.
XX
PR   12-JUN-1998;   98US-0089086P.
PR   12-JUN-1998;   98US-0089101P.
XX
PA   (NEWE ) NEW ENGLAND BIOLABS INC.
XX
PI   Raleigh EA,  Vaisvila R,  Morgan RD;
XX
DR   WPI; 2000-116558/10.
XX
PT   Cloning intact genes used to isolate genes for restriction enzymes.
XX
PS   Disclosure; Page 5; 97pp; English.
XX
CC   This invention describes a novel method for cloning intact, diversity-
CC   selected genes (I) from within gene cassettes (GC) which comprises
CC   identifying DNA repeats that flank GC, hybridizing oligonucleotides (ON)
CC   to these repeats and amplification to produce DNA fragments containing
CC   (I), ligating these fragments into a vector and transforming cells with
CC   the vector. This method is used to clone a wide variety of prokaryotic
CC   genes that provide a selective advantage under particular conditions,
CC   particularly those that encode restriction enzymes (used as reagents in
CC   molecular biology); adhesins (for use in coating or for targeting
CC   molecules or organisms to particular sites, e.g. for competitive
CC   exclusion of a selected pathogen); detoxifying enzymes; toxins that
CC   interact with a host, e.g. for synthesis of inhibitors or antagonists of
CC   the toxin, or in vaccination, or a modification methyltransferase. Intact
CC   genes can be cloned directly with a high probability that the orientation
CC   of expression is known in advance and low probability of association with
CC   extraneous, possibly toxic, genes. This sequence represents a VCR element
CC   inverse core DNA sequence isolated from Vibrio cholera
XX
SQ   Sequence 7 BP; 2 A; 1 C; 0 G; 0 T; 0 U; 4 Other;

  Query Match             30.0%;  Score 3;  DB 3;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          4 RRR 2


RESULT 87
AAZ88743
ID   AAZ88743 standard; DNA; 8 BP.
XX
AC   AAZ88743;
XX
DT   16-MAY-2000  (first entry)
XX
DE   V. cholera VCR element core DNA sequence.
XX
KW   Diversity-selected gene; restriction enzyme; adhesin; toxin;
KW   detoxifying enzyme; VCR element; ss.
XX
OS   Vibrio cholerae.
XX
PN   WO9964632-A1.
XX
PD   16-DEC-1999.
XX
PF   11-JUN-1999;   99WO-US013295.
XX
PR   12-JUN-1998;   98US-0089086P.
PR   12-JUN-1998;   98US-0089101P.
XX
PA   (NEWE ) NEW ENGLAND BIOLABS INC.
XX
PI   Raleigh EA,  Vaisvila R,  Morgan RD;
XX
DR   WPI; 2000-116558/10.
XX
PT   Cloning intact genes used to isolate genes for restriction enzymes.
XX
PS   Disclosure; Page 5; 97pp; English.
XX
CC   This invention describes a novel method for cloning intact, diversity-
CC   selected genes (I) from within gene cassettes (GC) which comprises
CC   identifying DNA repeats that flank GC, hybridizing oligonucleotides (ON)
CC   to these repeats and amplification to produce DNA fragments containing
CC   (I), ligating these fragments into a vector and transforming cells with
CC   the vector. This method is used to clone a wide variety of prokaryotic
CC   genes that provide a selective advantage under particular conditions,
CC   particularly those that encode restriction enzymes (used as reagents in
CC   molecular biology); adhesins (for use in coating or for targeting
CC   molecules or organisms to particular sites, e.g. for competitive
CC   exclusion of a selected pathogen); detoxifying enzymes; toxins that
CC   interact with a host, e.g. for synthesis of inhibitors or antagonists of
CC   the toxin, or in vaccination, or a modification methyltransferase. Intact
CC   genes can be cloned directly with a high probability that the orientation
CC   of expression is known in advance and low probability of association with
CC   extraneous, possibly toxic, genes. This sequence represents a VCR element
CC   core DNA sequence isolated from Vibrio cholera
XX
SQ   Sequence 8 BP; 0 A; 0 C; 1 G; 2 T; 0 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 3;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          4 RRR 6


RESULT 88
AAZ88743/c
ID   AAZ88743 standard; DNA; 8 BP.
XX
```

AC AAZ88743;
XX
DT 16-MAY-2000 (first entry)
XX
DE V. cholera VCR element core DNA sequence.
XX
KW Diversity-selected gene; restriction enzyme; adhesin; toxin;
KW detoxifying enzyme; VCR element; ss.
XX
OS Vibrio cholerae.
XX
PN WO9964632-A1.
XX
PD 16-DEC-1999.
XX
PF 11-JUN-1999; 99WO-US013295.
XX
PR 12-JUN-1998; 98US-0089086P.
PR 12-JUN-1998; 98US-0089101P.
XX
PA (NEWE) NEW ENGLAND BIOLABS INC.
XX
PI Raleigh EA, Vaisvila R, Morgan RD;
XX
DR WPI; 2000-116558/10.
XX
PT Cloning intact genes used to isolate genes for restriction enzymes.
XX
PS Disclosure; Page 5; 97pp; English.
XX
CC This invention describes a novel method for cloning intact, diversity-
CC selected genes (I) from within gene cassettes (GC) which comprises
CC identifying DNA repeats that flank GC, hybridizing oligonucleotides (ON)
CC to these repeats and amplification to produce DNA fragments containing
CC (I), ligating these fragments into a vector and transforming cells with
CC the vector. This method is used to clone a wide variety of prokaryotic
CC genes that provide a selective advantage under particular conditions,
CC particularly those that encode restriction enzymes (used as reagents in
CC molecular biology); adhesins (for use in coating or for targeting
CC molecules or organisms to particular sites, e.g. for competitive
CC exclusion of a selected pathogen); detoxifying enzymes; toxins that
CC interact with a host, e.g. for synthesis of inhibitors or antagonists of
CC the toxin, or in vaccination, or a modification methyltransferase. Intact
CC genes can be cloned directly with a high probability that the orientation
CC of expression is known in advance and low probability of association with
CC extraneous, possibly toxic, genes. This sequence represents a VCR element
CC core DNA sequence isolated from Vibrio cholera
XX
SQ Sequence 8 BP; 0 A; 0 C; 1 G; 2 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          8 YYY 10
              |||
Db          7 YYY 5
```

RESULT 89
AAA28439
ID AAA28439 standard; DNA; 8 BP.
XX
AC AAA28439;
XX
DT 29-AUG-2000 (first entry)
XX
DE Synthetic promoter conserved domain IIa.
XX
KW Artificial promoter; strong; weak; transgene expression; plant; ss.
XX
OS Synthetic.
XX
PN EP1002869-A1.
XX
PD 24-MAY-2000.
XX
PF 25-FEB-1999; 99EP-00301419.
XX
PR 09-NOV-1998; 98IN-DE003322.
XX
PA (COUL) CSIR COUNCIL SCI IND RES.
XX
PI Tuli R, Sawant SV, Singh PK, Gupta SK;
XX
DR WPI; 2000-341712/30.
XX
PT New chemically synthesized artificial promoter, useful high level
PT expression of transgenes in different organisms.
XX
PS Claim 6; Page 17; 40pp; English.
XX
CC A chemically synthesized promoter can comprise a conserved domain IIa as
CC shown here for high level expression of genes. The sequence comprises a
CC tandem repeat of 2-8 nucleotides comprising A/G nucleotides. These
CC elements are present beyond position -200 of the promoter. Chemically
CC synthesized artificial promoters are new and comprise a DNA sequence
CC designed for a targeted level and pattern of gene expression by
CC strategically putting together several signature sequences identified by
CC sequence alignment and statistical analysis of a large database
CC constructed for this purpose. A method for chemically synthesizing an
CC artificial promoter for expressing genes at a desired level in different
CC organisms is also claimed. The high level expression in a plant using
CC such an artificial promoter (e.g. AAA28449) can be measured comprising
CC polyethylene glycol (PEG) mediated transformation of plant protoplasts as
CC well as biolistic mediated transformation of plant tissues including
CC root, stem, intact leaf tissue followed by transient GUS assay to compare
CC with a natural CaMV 35S promoter showing the desired level of activity.
CC The promoter is useful for high level expression of transgenes in
CC different organisms and for testing high level gene expression in plants
CC (claimed). The promoter is biologically active and is efficient and can
CC be synthesized to express in even the most complex organisms
XX
SQ Sequence 8 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RRR 3
              |||
Db          1 RRR 3
```

RESULT 90
AAA28439/c
ID AAA28439 standard; DNA; 8 BP.
XX
AC AAA28439;
XX
DT 29-AUG-2000 (first entry)
XX
DE Synthetic promoter conserved domain IIa.
XX
KW Artificial promoter; strong; weak; transgene expression; plant; ss.
XX
OS Synthetic.
XX
PN EP1002869-A1.
XX
PD 24-MAY-2000.
XX
PF 25-FEB-1999; 99EP-00301419.
XX
PR 09-NOV-1998; 98IN-DE003322.
XX

PA (COUL) CSIR COUNCIL SCI IND RES.
XX
PI Tuli R, Sawant SV, Singh PK, Gupta SK;
XX
DR WPI; 2000-341712/30.
XX
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PT expression of transgenes in different organisms.
XX
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XX
CC A chemically synthesized promoter can comprise a conserved domain IIa as
CC shown here for high level expression of genes. The sequence comprises a
CC tandem repeat of 2-8 nucleotides comprising A/G nucleotides. These
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CC synthesized artificial promoters are new and comprise a DNA sequence
CC designed for a targeted level and pattern of gene expression by
CC strategically putting together several signature sequences identified by
CC sequence alignment and statistical analysis of a large database
CC constructed for this purpose. A method for chemically synthesizing an
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CC organisms is also claimed. The high level expression in a plant using
CC such an artificial promoter (e.g. AAA28449) can be measured comprising
CC polyethylene glycol (PEG) mediated transformation of plant protoplasts as
CC well as biolistic mediated transformation of plant tissues including
CC root, stem, intact leaf tissue followed by transient GUS assay to compare
CC with a natural CaMV 35S promoter showing the desired level of activity.
CC The promoter is useful for high level expression of transgenes in
CC different organisms and for testing high level gene expression in plants
CC (claimed). The promoter is biologically active and is efficient and can
CC be synthesized to express in even the most complex organisms
XX
SQ Sequence 8 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 8 YYY 6

RESULT 91
AAQ63868
ID AAQ63868 standard; DNA; 9 BP.
XX
AC AAQ63868;
XX
DT 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
DE Haematopoietic cell factor binding motif from human R gene 5'-UTR.
XX
KW Immunoglobulin; IgG receptor; gamma-interferon activation; g-IFN;
KW haematopoietic cell; protein factor; binding site; GRR motif;
KW human high affinity Fc receptor for IgG; human Fc gamma R1; R gene;
KW DNA response element; MATE motif; GIRE motif; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN FR2696181-A1.
XX
PD 01-APR-1994.
XX
PF 25-SEP-1992; 92FR-00011498.
XX
PR 25-SEP-1992; 92FR-00011498.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Benech P, Perez C, Wietzerbin J;
XX
DR WPI; 1994-128281/16.
XX
PT New nucleotide sequences are specific target for proteins exclusive to
PT haematopoietic cells - used to impart, to partic. cells, a response to
PT gamma-interferon, e.g. for gene therapy.
XX
PS Claim 3; Page 25; 37pp; French.
XX
CC The region immediately upstream of the sequence which codes for the human
CC high affinity Fc receptor for IgG (the R gene) contains binding sites
CC specific for haematopoietic cells, including the response element
CC sequence AAQ63868. One or more copies of this sequence is preferred for
CC conferring on a gene a transcriptional activity limited to haematopoietic
CC cells. The DNA motif thus has potential in gene therapy. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 9 BP; 0 A; 1 C; 0 G; 4 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 92
AAQ63868/c
ID AAQ63868 standard; DNA; 9 BP.
XX
AC AAQ63868;
XX
DT 25-MAR-2003 (revised)
DT 10-NOV-1994 (first entry)
XX
DE Haematopoietic cell factor binding motif from human R gene 5'-UTR.
XX
KW Immunoglobulin; IgG receptor; gamma-interferon activation; g-IFN;
KW haematopoietic cell; protein factor; binding site; GRR motif;
KW human high affinity Fc receptor for IgG; human Fc gamma R1; R gene;
KW DNA response element; MATE motif; GIRE motif; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN FR2696181-A1.
XX
PD 01-APR-1994.
XX
PF 25-SEP-1992; 92FR-00011498.
XX
PR 25-SEP-1992; 92FR-00011498.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Benech P, Perez C, Wietzerbin J;
XX
DR WPI; 1994-128281/16.
XX
PT New nucleotide sequences are specific target for proteins exclusive to
PT haematopoietic cells - used to impart, to partic. cells, a response to
PT gamma-interferon, e.g. for gene therapy.
XX
PS Claim 3; Page 25; 37pp; French.
XX
CC The region immediately upstream of the sequence which codes for the human
CC high affinity Fc receptor for IgG (the R gene) contains binding sites
CC specific for haematopoietic cells, including the response element
CC sequence AAQ63868. One or more copies of this sequence is preferred for
CC conferring on a gene a transcriptional activity limited to haematopoietic
CC cells. The DNA motif thus has potential in gene therapy. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX

```
SQ   Sequence 9 BP; 0 A; 1 C; 0 G; 4 T; 0 U; 4 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          3 RRR 1


RESULT 93
AAT96075
ID   AAT96075 standard; DNA; 9 BP.
XX
AC   AAT96075;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
PI   Jurka JW;
XX
DR   WPI; 1998-041303/04.
XX
PT   Genomic integration of DNA by site directed recombination - using
PT   construct containing recombination region homologous to consensus defined
PT   flanking region of short interspersed repeated DNA element.
XX
PS   Claim 7; Col 15-16; 12pp; English.
XX
CC   Integrating a DNA sequence into the genome of a vertebrate host cell,
CC   comprises introducing a construct comprising the DNA sequence and a
CC   recombination region homologous to a consensus defined flanking region of
CC   a short interspersed repeated DNA element (SINE), e.g. the present
CC   sequence. The method may be used to modify the phenotype of cells, or
CC   investigate the response of receptors, metabolic pathways or expression
CC   products involved in the regulation of transcription or transduction of
CC   signals. It may also be used to produce protein products and transgenic
CC   animals, by providing novel capabilities to the cells or inhibiting
CC   endogenous capabilities, investigate physiological indications and screen
CC   cosmetics, foods and drugs. By using antisense sequences effective
CC   inhibition of both copies of a gene is possible, ensuring the substantial
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 9 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          6 RRR 8


RESULT 94
AAT96075/c
ID   AAT96075 standard; DNA; 9 BP.
XX
AC   AAT96075;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
PI   Jurka JW;
XX
DR   WPI; 1998-041303/04.
XX
PT   Genomic integration of DNA by site directed recombination - using
PT   construct containing recombination region homologous to consensus defined
PT   flanking region of short interspersed repeated DNA element.
XX
PS   Claim 7; Col 15-16; 12pp; English.
XX
CC   Integrating a DNA sequence into the genome of a vertebrate host cell,
CC   comprises introducing a construct comprising the DNA sequence and a
CC   recombination region homologous to a consensus defined flanking region of
CC   a short interspersed repeated DNA element (SINE), e.g. the present
CC   sequence. The method may be used to modify the phenotype of cells, or
CC   investigate the response of receptors, metabolic pathways or expression
CC   products involved in the regulation of transcription or transduction of
CC   signals. It may also be used to produce protein products and transgenic
CC   animals, by providing novel capabilities to the cells or inhibiting
CC   endogenous capabilities, investigate physiological indications and screen
CC   cosmetics, foods and drugs. By using antisense sequences effective
CC   inhibition of both copies of a gene is possible, ensuring the substantial
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 9 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          8 YYY 6


RESULT 95
AAQ31609
ID   AAQ31609 standard; DNA; 10 BP.
XX
AC   AAQ31609;
XX
DT   25-MAR-2003  (revised)
DT   02-APR-1993  (first entry)
XX
DE   Cauliflower mosaic virus 35S enhancer sequence.
XX
```

KW CaMV; transcription initiation rate; enhancement; variation; ss.
XX
OS Cauliflower mosaic virus.
XX
PN US5164316-A.
XX
PD 17-NOV-1992.
XX
PF 17-AUG-1989; 89US-00395155.
XX
PR 13-JAN-1987; 87US-00002780.
PR 25-JAN-1988; 88US-00147887.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Mcpherson JC, Kay R;
XX
DR WPI; 1992-407146/49.
XX
PT New plant cell comprising DNA contg. duplicated cauliflower mosaic virus
PT 35 S enhancer sequence - used to provide enhanced transcription
PT initiation rate.
XX
PS Disclosure; Page 7; 12pp; English.
XX
CC The sequence is that of a cauliflower mosaic virus 35S enhancer sequence
CC which can be used in a DNA construct which permits variation in
CC enhancement of the transcription initiation rate in the plant cell. This
CC allows the prodn. of new characteristics in transformed plants, e.g.
CC increased prodn. of proteins for agronomical or commercial purposes when
CC the construct contains a protein-coding sequence, or the regulation of
CC exogenous gene expression by competing levels of antisense RNA. (Updated
CC on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7
|||
Db 8 WWG 10

RESULT 96
AAQ31609/c
ID AAQ31609 standard; DNA; 10 BP.
XX
AC AAQ31609;
XX
DT 25-MAR-2003 (revised)
DT 02-APR-1993 (first entry)
XX
DE Cauliflower mosaic virus 35S enhancer sequence.
XX
KW CaMV; transcription initiation rate; enhancement; variation; ss.
XX
OS Cauliflower mosaic virus.
XX
PN US5164316-A.
XX
PD 17-NOV-1992.
XX
PF 17-AUG-1989; 89US-00395155.
XX
PR 13-JAN-1987; 87US-00002780.
PR 25-JAN-1988; 88US-00147887.
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI Mcpherson JC, Kay R;
XX
DR WPI; 1992-407146/49.
XX
PT New plant cell comprising DNA contg. duplicated cauliflower mosaic virus
PT 35 S enhancer sequence - used to provide enhanced transcription
PT initiation rate.
XX
PS Disclosure; Page 7; 12pp; English.
XX
CC The sequence is that of a cauliflower mosaic virus 35S enhancer sequence
CC which can be used in a DNA construct which permits variation in
CC enhancement of the transcription initiation rate in the plant cell. This
CC allows the prodn. of new characteristics in transformed plants, e.g.
CC increased prodn. of proteins for agronomical or commercial purposes when
CC the construct contains a protein-coding sequence, or the regulation of
CC exogenous gene expression by competing levels of antisense RNA. (Updated
CC on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
|||
Db 10 CWW 8

RESULT 97
AAQ30505
ID AAQ30505 standard; DNA; 10 BP.
XX
AC AAQ30505;
XX
DT 25-MAR-2003 (revised)
DT 19-MAR-1993 (first entry)
XX
DE Serum response element under control of TCRE.
XX
KW Transcriptional control recognition element; decoy; cellular RNA;
KW promoter; hormone receptor element; viral; liver; tissue; viral;
KW proliferation; linker; NF-1; ss.
XX
OS Synthetic.
XX
PN WO9218522-A1.
XX
PD 29-OCT-1992.
XX
PF 17-APR-1992; 92WO-US003205.
XX
PR 18-APR-1991; 91US-00687337.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chu BC, Orgel L;
XX
DR WPI; 1992-382035/46.
XX
PT New oligo-nucleotide(s) contg. transcription control recognition element
PT - stabilised by covalent bonding of two DNA strands, act as decoys for
PT regulatory protein to modulate specific RNA.
XX
PS Disclosure; Page 6; 41pp; English.
XX
CC Transcriptional control recognition element recognition sequences may be
CC recognised by control proteins and are involved in either enhancing or
CC repressing transcription of associated sequences. TCR sequences include
CC promoter elements, hormone receptor elements, viral, cellular, liver or
CC tissue elements, etc. The sequence represents an exemplary general
CC element, the serum response element. A typical application of the TCRE
CC recognising oligonucleotides is inhibition of viral proliferation. See
CC also AAQ30472-518. (Updated on 25-MAR-2003 to correct PN field.)

```
XX
SQ   Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 98
AAQ30505/c
ID   AAQ30505 standard; DNA; 10 BP.
XX
AC   AAQ30505;
XX
DT   25-MAR-2003  (revised)
DT   19-MAR-1993  (first entry)
XX
DE   Serum response element under control of TCRE.
XX
KW   Transcriptional control recognition element; decoy; cellular RNA;
KW   promoter; hormone receptor element; viral; liver; tissue; viral;
KW   proliferation; linker; NF-1; ss.
XX
OS   Synthetic.
XX
PN   WO9218522-A1.
XX
PD   29-OCT-1992.
XX
PF   17-APR-1992;   92WO-US003205.
XX
PR   18-APR-1991;   91US-00687337.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Chu BC,  Orgel L;
XX
DR   WPI; 1992-382035/46.
XX
PT   New oligo-nucleotide(s) contg. transcription control recognition element
PT   - stabilised by covalent bonding of two DNA strands, act as decoys for
PT   regulatory protein to modulate specific RNA.
XX
PS   Disclosure; Page 6; 41pp; English.
XX
CC   Transcriptional control recognition element recognition sequences may be
CC   recognised by control proteins and are involved in either enhancing or
CC   repressing transcription of associated sequences. TCR sequences include
CC   promoter elements, hormone receptor elements, viral, cellular, liver or
CC   tissue elements, etc. The sequence represents an exemplary general
CC   element, the serum response element. A typical application of the TCRE
CC   recognising oligonucleotides is inhibition of viral proliferation. See
CC   also AAQ30472-518. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7


RESULT 99
AAQ38817
ID   AAQ38817 standard; DNA; 10 BP.
XX
AC   AAQ38817;
XX
DT   25-MAR-2003  (revised)
DT   27-JUL-1993  (first entry)
XX
DE   CaMV 35S promoter repeat unit.
XX
KW   Cauliflower mosaic virus; enhancer; construct; ss.
XX
OS   Synthetic.
XX
PN   US5196525-A.
XX
PD   23-MAR-1993.
XX
PF   08-APR-1991;   91US-00682049.
XX
PR   13-JAN-1987;   87US-00002780.
PR   25-JAN-1988;   88US-00147887.
PR   17-AUG-1989;   89US-00395155.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Mcpherson JC,  Kay R;
XX
DR   WPI; 1993-116860/14.
XX
PT   DNA construct for varying transcription initiation rate enhancement in
PT   plants - comprises transcription initiation region with tandem duplicated
PT   cauliflower mosaic virus 35-S enhancer sequence, nucleotide sequence, and
PT   termination region.
XX
PS   Disclosure; Page 7; 12pp; English.
XX
CC   The sequence represents a single repeat unit of the CaMV 35S promoter.
CC   Synthetic enhancer domains comprise a plurality of the units of the
CC   natural enhancer spaced in the same was as in the natural enhancer. The
CC   synthetic enhancer doamins may be used in DNA constructs which allow for
CC   increased rate of transcription. These constructs have wide application
CC   in the control of the formation of expression prods. and protection
CC   against pathogens or antibiotics, etc. See also AAQ38816. (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          8 WWG 10


RESULT 100
AAQ38817/c
ID   AAQ38817 standard; DNA; 10 BP.
XX
AC   AAQ38817;
XX
DT   25-MAR-2003  (revised)
DT   27-JUL-1993  (first entry)
XX
DE   CaMV 35S promoter repeat unit.
XX
KW   Cauliflower mosaic virus; enhancer; construct; ss.
XX
OS   Synthetic.
XX
PN   US5196525-A.
XX
PD   23-MAR-1993.
XX
```

```
PF   08-APR-1991;   91US-00682049.
XX
PR   13-JAN-1987;   87US-00002780.
PR   25-JAN-1988;   88US-00147887.
PR   17-AUG-1989;   89US-00395155.
XX
PA   (UYBR-) UNIV BRITISH COLUMBIA.
XX
PI   Mcpherson JC,  Kay R;
XX
DR   WPI; 1993-116860/14.
XX
PT   DNA construct for varying transcription initiation rate enhancement in
PT   plants - comprises transcription initiation region with tandem duplicated
PT   cauliflower mosaic virus 35-S enhancer sequence, nucleotide sequence, and
PT   termination region.
XX
PS   Disclosure; Page 7; 12pp; English.
XX
CC   The sequence represents a single repeat unit of the CaMV 35S promoter.
CC   Synthetic enhancer domains comprise a plurality of the units of the
CC   natural enhancer spaced in the same was as in the natural enhancer. The
CC   synthetic enhancer doamins may be used in DNA constructs which allow for
CC   increased rate of transcription. These constructs have wide application
CC   in the control of the formation of expression prods. and protection
CC   against pathogens or antibiotics, etc. See also AAQ38816. (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db         10 CWW 8


RESULT 101
AAQ72970
ID   AAQ72970 standard; DNA; 10 BP.
XX
AC   AAQ72970;
XX
DT   25-MAR-2003  (revised)
DT   30-JUN-1995  (first entry)
XX
DE   Engineered enhancer element repeat unit in CaMV35S promoter.
XX
KW   Enhancer element; repeat unit; promoter; cauliflower mosaic virus;
KW   CaMV35S; enhancer region; core sequence; variability; transgenic; plant;
KW   expression; foreign gene; pathogen; antibiotic; ss.
XX
OS   Synthetic.
XX
PN   US5359142-A.
XX
PD   25-OCT-1994.
XX
PF   09-MAR-1994;   94US-00209752.
XX
PR   13-JAN-1987;   87US-00002780.
PR   25-JAN-1988;   88US-00147887.
PR   17-AUG-1989;   89US-00395155.
PR   17-NOV-1992;   92US-00977600.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Kay R,  Mcpherson JC;
XX
DR   WPI; 1994-341080/42.
XX
PT   Novel differentiated plants contg improved DNA constructs - with
PT   engineered enhancer element to enhance expression of foreign genes.
XX
PS   Disclosure; Col 3; 11pp; English.
XX
CC   The sequence of a modified enhancer sequence used to construct a
CC   heterologous enhancer/promoter region for the improved expression of
CC   genes under control of the modified enhancer promoter in plants. The
CC   engineered enhancer region may contain portions of the sequence shown, at
CC   least the sequence GTGG or its complementary sequence. The promoter may
CC   the 35S promoter of the cauliflower mosaic virus (CaMV35S) or a
CC   heterologous promoter e.g. the T DNA gene 5 or 7 promoter. The engineered
CC   enhancer/promoter preferably has an enhancer domain with one more repeat
CC   than the 35S enhancer. The natural enhancer sequence can be repeated
CC   several times in the enhancer region. The repeats can comprise of 4-16
CC   bases, generally 4, 7, or 10 base repeats. The repeat structure may be
CC   imperfect, containing a core sequence surrounded by regions of
CC   variability. Transgenic plants show increased expression of foreign genes
CC   due to the presence of the engineered enhancer sequences. The improved
CC   contructions have wide applications e.g. in the control of the formation
CC   of products, protection against pathogens or antibiotics. (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          8 WWG 10


RESULT 102
AAQ72970/c
ID   AAQ72970 standard; DNA; 10 BP.
XX
AC   AAQ72970;
XX
DT   25-MAR-2003  (revised)
DT   30-JUN-1995  (first entry)
XX
DE   Engineered enhancer element repeat unit in CaMV35S promoter.
XX
KW   Enhancer element; repeat unit; promoter; cauliflower mosaic virus;
KW   CaMV35S; enhancer region; core sequence; variability; transgenic; plant;
KW   expression; foreign gene; pathogen; antibiotic; ss.
XX
OS   Synthetic.
XX
PN   US5359142-A.
XX
PD   25-OCT-1994.
XX
PF   09-MAR-1994;   94US-00209752.
XX
PR   13-JAN-1987;   87US-00002780.
PR   25-JAN-1988;   88US-00147887.
PR   17-AUG-1989;   89US-00395155.
PR   17-NOV-1992;   92US-00977600.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Kay R,  Mcpherson JC;
XX
DR   WPI; 1994-341080/42.
XX
PT   Novel differentiated plants contg improved DNA constructs - with
PT   engineered enhancer element to enhance expression of foreign genes.
XX
PS   Disclosure; Col 3; 11pp; English.
XX
```

```
CC   The sequence of a modified enhancer sequence used to construct a
CC   heterologous enhancer/promoter region for the improved expression of
CC   genes under control of the modified enhancer promoter in plants. The
CC   engineered enhancer region may contain portions of the sequence shown, at
CC   least the sequence GTGG or its complementary sequence. The promoter may
CC   the 35S promoter of the cauliflower mosaic virus (CaMV35S) or a
CC   heterologous promoter e.g. the T DNA gene 5 or 7 promoter. The engineered
CC   enhancer/promoter preferably has an enhancer domain with one more repeat
CC   than the 35S enhancer. The natural enhancer sequence can be repeated
CC   several times in the enhancer region. The repeats can comprise of 4-16
CC   bases, generally 4, 7, or 10 base repeats. The repeat structure may be
CC   imperfect, containing a core sequence surrounded by regions of
CC   variability. Transgenic plants show increased expression of foreign genes
CC   due to the presence of the engineered enhancer sequences. The improved
CC   contructions have wide applications e.g. in the control of the formation
CC   of products, protection against pathogens or antibiotics. (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db         10 CWW 8


RESULT 103
AAQ81756
ID   AAQ81756 standard; DNA; 10 BP.
XX
AC   AAQ81756;
XX
DT   25-MAR-2003  (revised)
DT   27-FEB-1995  (first entry)
XX
DE   CaMV 35S enhancer repetitive unit.
XX
KW   CaMV; enhancer; promoter; repetitive unit; transcription; initiation; ss.
XX
OS   Cauliflower mosaic virus.
XX
PN   US5322938-A.
XX
PD   21-JUN-1994.
XX
PF   17-NOV-1992;   92US-00977600.
XX
PR   13-JAN-1987;   87US-00002780.
PR   25-JAN-1988;   88US-00147887.
PR   17-AUG-1989;   89US-00395155.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Mcpherson JC,  Kay R;
XX
DR   WPI; 1994-199579/24.
XX
PT   Transcription initiation regions with enhanced transcription efficiency -
PT   comprise tandemly duplicated CaMV 35S enhancer sequences and a promoter.
XX
PS   Disclosure; Col 3; 12pp; English.
XX
CC   Many viral, plant and animal enhancers contain sets of repeated sequence
CC   elements, such as the sequences given in AAQ81755-56. These units are
CC   repeated several times within the upstream sequence of the CaMV 35S
CC   promoter region. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          8 WWG 10


RESULT 104
AAQ81756/c
ID   AAQ81756 standard; DNA; 10 BP.
XX
AC   AAQ81756;
XX
DT   25-MAR-2003  (revised)
DT   27-FEB-1995  (first entry)
XX
DE   CaMV 35S enhancer repetitive unit.
XX
KW   CaMV; enhancer; promoter; repetitive unit; transcription; initiation; ss.
XX
OS   Cauliflower mosaic virus.
XX
PN   US5322938-A.
XX
PD   21-JUN-1994.
XX
PF   17-NOV-1992;   92US-00977600.
XX
PR   13-JAN-1987;   87US-00002780.
PR   25-JAN-1988;   88US-00147887.
PR   17-AUG-1989;   89US-00395155.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Mcpherson JC,  Kay R;
XX
DR   WPI; 1994-199579/24.
XX
PT   Transcription initiation regions with enhanced transcription efficiency -
PT   comprise tandemly duplicated CaMV 35S enhancer sequences and a promoter.
XX
PS   Disclosure; Col 3; 12pp; English.
XX
CC   Many viral, plant and animal enhancers contain sets of repeated sequence
CC   elements, such as the sequences given in AAQ81755-56. These units are
CC   repeated several times within the upstream sequence of the CaMV 35S
CC   promoter region. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 10 BP; 0 A; 0 C; 5 G; 2 T; 0 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db         10 CWW 8


RESULT 105
AAT96065
ID   AAT96065 standard; DNA; 10 BP.
XX
AC   AAT96065;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
```

OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 11-12; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 10 BP; 3 A; 0 C; 0 G; 2 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 7 YYY 9

RESULT 106
AAT96065/c
ID AAT96065 standard; DNA; 10 BP.
XX
AC AAT96065;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 11-12; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 10 BP; 3 A; 0 C; 0 G; 2 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 9 RRR 7

RESULT 107
AAT96076
ID AAT96076 standard; DNA; 10 BP.
XX
AC AAT96076;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 7; Col 15-16; 12pp; English.
XX

CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 10 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
||| |
Db 7 RRR 9

RESULT 108
AAT96076/c
ID AAT96076 standard; DNA; 10 BP.
XX
AC AAT96076;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 7; Col 15-16; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 10 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
||| |
Db 9 YYY 7

RESULT 109
AAX88060
ID AAX88060 standard; cDNA; 10 BP.
XX
AC AAX88060;
XX
DT 08-SEP-1999 (first entry)
XX
DE Serum response factor inner core DNA.
XX
KW Plasmid pIG0100A; plasmid pIG0335; expression vector; treatment; disease;
KW RNA stability element; gene therapy; muscle atrophy; neurological;
KW muscular disease; systemic disease; aging; trophic factor; haemophilia;
KW clotting factor; atherogenesis; atherosclerotic; cardiovascular;
KW cerebrovascular; peripheral-vascular disease; hormone deficiency;
KW diabetes; transgenic animal; carcinogen; regulatory element;
KW livestock improvement; immune response; ss.
XX
OS Unidentified.
XX
PN US5925564-A.
XX
PD 20-JUL-1999.
XX
PF 07-JUN-1995; 95US-00472809.
XX
PR 06-NOV-1991; 91US-00789919.
PR 09-MAR-1994; 94US-00209846.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI O'malley BW, Demayo FJ, Schwartz RJ;
XX
DR WPI; 1999-418276/35.
XX
PT New expression vector system useful for gene therapy.
XX
PS Disclosure; Col 39-40; 67pp; English.
XX
CC This invention describes novel expression vector systems containing RNA
CC stability elements from 3' flanking sequences used for establishing
CC expression of a nucleic acid sequence within a tissue. The vectors also
CC facilitate enhanced expression in tissues and target expression with
CC tissue specificity. The expression vectors can be used to treat diseases
CC through gene therapy by targeting the vector to specific tissues.
CC Diseases that can be treated include muscle atrophy associated with
CC neurological, muscular or systemic disease, aging by causing tissues to
CC express trophic factors, haemophilia by causing tissues to express and
CC secrete clotting factor into the circulation, atherogenesis and
CC atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular
CC disease by causing tissues to express factors involved in tissue
CC metabolism. They can be used to replace genes of inherited genetic
CC defects or acquired hormone deficiencies e.g. diabetes. To transform
CC cells to produce particular proteins or RNA in vitro. To create
CC transgenic animals which can be used for research into human diseases,
CC assessing novel therapeutic methods, assessing the effect of chemical and
CC physical carcinogens and for studying the effect of genes and genetic

```
CC   regulatory elements or livestock improvement. They can be used to induce
CC   an immune response. These vectors provide controlled expression of the
CC   genes they carry and produce a significantly high level of expression.
CC   Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the
CC   vectors which causes increased expression
XX
SQ   Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 110
AAX88060/c
ID   AAX88060 standard; cDNA; 10 BP.
XX
AC   AAX88060;
XX
DT   08-SEP-1999  (first entry)
XX
DE   Serum response factor inner core DNA.
XX
KW   Plasmid pIG0100A; plasmid pIG0335; expression vector; treatment; disease;
KW   RNA stability element; gene therapy; muscle atrophy; neurological;
KW   muscular disease; systemic disease; aging; trophic factor; haemophilia;
KW   clotting factor; atherogenesis; atherosclerotic; cardiovascular;
KW   cerebrovascular; peripheral-vascular disease; hormone deficiency;
KW   diabetes; transgenic animal; carcinogen; regulatory element;
KW   livestock improvement; immune response; ss.
XX
OS   Unidentified.
XX
PN   US5925564-A.
XX
PD   20-JUL-1999.
XX
PF   07-JUN-1995;   95US-00472809.
XX
PR   06-NOV-1991;   91US-00789919.
PR   09-MAR-1994;   94US-00209846.
XX
PA   (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI   O'malley BW,  Demayo FJ,  Schwartz RJ;
XX
DR   WPI; 1999-418276/35.
XX
PT   New expression vector system useful for gene therapy.
XX
PS   Disclosure; Col 39-40; 67pp; English.
XX
CC   This invention describes novel expression vector systems containing RNA
CC   stability elements from 3' flanking sequences used for establishing
CC   expression of a nucleic acid sequence within a tissue. The vectors also
CC   facilitate enhanced expression in tissues and target expression with
CC   tissue specificity. The expression vectors can be used to treat diseases
CC   through gene therapy by targeting the vector to specific tissues.
CC   Diseases that can be treated include muscle atrophy associated with
CC   neurological, muscular or systemic disease, aging by causing tissues to
CC   express trophic factors, haemophilia by causing tissues to express and
CC   secrete clotting factor into the circulation, atherogenesis and
CC   atherosclerotic cardiovascular, cerebrovascular or peripheral-vascular
CC   disease by causing tissues to express factors involved in tissue
CC   metabolism. They can be used to replace genes of inherited genetic
CC   defects or acquired hormone deficiencies e.g. diabetes. To transform
CC   cells to produce particular proteins or RNA in vitro. To create
CC   transgenic animals which can be used for research into human diseases,
CC   assessing novel therapeutic methods, assessing the effect of chemical and
CC   physical carcinogens and for studying the effect of genes and genetic
CC   regulatory elements or livestock improvement. They can be used to induce
CC   an immune response. These vectors provide controlled expression of the
CC   genes they carry and produce a significantly high level of expression.
CC   Using 3'UTR sequences reduces the decay rates of the mRNAs encoded by the
CC   vectors which causes increased expression
XX
SQ   Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7


RESULT 111
AAA91882
ID   AAA91882 standard; DNA; 10 BP.
XX
AC   AAA91882;
XX
DT   08-JAN-2001  (first entry)
XX
DE   Complement of SNP site beginning at position 546 of the TGFb-RII gene.
XX
KW   TGFb-RII; promoter; gene therapy; end-stage renal disease; ESRD;
KW   single nucleotide polymorphism; SNP; human; primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(7,T)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200049169-A1.
XX
PD   24-AUG-2000.
XX
PF   18-FEB-2000; 2000WO-US004251.
XX
PR   19-FEB-1999;   99US-0120787P.
XX
PA   (DZGE-) DZGENES LLC.
XX
PI   Moskowitz DW;
XX
DR   WPI; 2000-549279/50.
XX
PT   Diagnosing genetic susceptibility for end-stage renal disease using
PT   single nucleotide polymorphisms, involves analyzing sample obtained from
PT   subject to detect genetic polymorphism in the sample polynucleotide.
XX
PS   Example 4; Page 38; 73pp; English.
XX
CC   The present invention relates the diagnosis of genetic susceptibility for
CC   end-stage renal disease (ESRD). The method involves analysing a
CC   polynucleotide sample for a single nucleotide polymorphism (SNP)
CC   associated with an altered susceptibility for ESRD. The method allows
CC   early detection of ESRD and hence effective delay or ideally, prevention
CC   of ESRD is made possible. The present sequence is a SNP site found in the
CC   human TGFb-RII promoter sequence (see AAA91867). Polymorphisms in this
CC   gene are known to be a probable trigger for renal apoptosis
XX
SQ   Sequence 10 BP; 0 A; 3 C; 1 G; 1 T; 0 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          3 RCW 5
              |||
Db          2 RCW 4


RESULT 112
AAA91882/c
ID   AAA91882 standard; DNA; 10 BP.
XX
AC   AAA91882;
XX
DT   08-JAN-2001  (first entry)
XX
DE   Complement of SNP site beginning at position 546 of the TGFb-RII gene.
XX
KW   TGFb-RII; promoter; gene therapy; end-stage renal disease; ESRD;
KW   single nucleotide polymorphism; SNP; human; primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(7,T)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200049169-A1.
XX
PD   24-AUG-2000.
XX
PF   18-FEB-2000; 2000WO-US004251.
XX
PR   19-FEB-1999;   99US-0120787P.
XX
PA   (DZGE-) DZGENES LLC.
XX
PI   Moskowitz DW;
XX
DR   WPI; 2000-549279/50.
XX
PT   Diagnosing genetic susceptibility for end-stage renal disease using
PT   single nucleotide polymorphisms, involves analyzing sample obtained from
PT   subject to detect genetic polymorphism in the sample polynucleotide.
XX
PS   Example 4; Page 38; 73pp; English.
XX
CC   The present invention relates the diagnosis of genetic susceptibility for
CC   end-stage renal disease (ESRD). The method involves analysing a
CC   polynucleotide sample for a single nucleotide polymorphism (SNP)
CC   associated with an altered susceptibility for ESRD. The method allows
CC   early detection of ESRD and hence effective delay or ideally, prevention
CC   of ESRD is made possible. The present sequence is a SNP site found in the
CC   human TGFb-RII promoter sequence (see AAA91867). Polymorphisms in this
CC   gene are known to be a probable trigger for renal apoptosis
XX
SQ   Sequence 10 BP; 0 A; 3 C; 1 G; 1 T; 0 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WGY 8
              |||
Db          4 WGY 2


RESULT 113
AAA16552
ID   AAA16552 standard; DNA; 10 BP.
XX
AC   AAA16552;
XX
DT   16-JUN-2000  (first entry)
XX
DE   Initiator consensus sequence SEQ ID NO:23.
XX
KW   Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW   oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW   MN/CA IX isoenzyme; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   US6027887-A.
XX
PD   22-FEB-2000.
XX
PF   24-JAN-1997;   97US-00787739.
XX
PR   21-OCT-1992;   92US-00964589.
PR   30-DEC-1993;   93US-00177093.
PR   15-JUN-1994;   94US-00260190.
PR   07-JUN-1995;   95US-00477504.
PR   07-JUN-1995;   95US-00481658.
PR   07-JUN-1995;   95US-00485049.
PR   07-JUN-1995;   95US-00485862.
PR   07-JUN-1995;   95US-00485863.
PR   07-JUN-1995;   95US-00486756.
PR   07-JUN-1995;   95US-00487077.
XX
PA   (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
XX
PI   Pastorek J,  Zavada J,  Pastorekova S;
XX
DR   WPI; 2000-194827/17.
XX
PT   Nucleic acid based assay for diagnosing a wide variety of
PT   preneoplastic/neoplastic disease comprises screening for the presence of
PT   abnormal MN gene expression in a vertebrate.
XX
PS   Disclosure; Col 85; 87pp; English.
XX
CC   The present invention describes a method of screening for
CC   preneoplastic/neoplastic disease. The method comprises: (1) determining
CC   whether abnormal MN gene expression is present in a vertebrate; and (2)
CC   if abnormal MN gene expression is determined to be present in the
CC   vertebrate, determining that the vertebrate has a significant risk of
CC   having preneoplastic/neoplastic disease. The MN gene is an oncogene and
CC   encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
CC   protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC   is used for detecting a wide variety of preneoplastic/neoplastic diseases
CC   in a vertebrate, preferably a human. The disease detected is mammary,
CC   bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC   vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
CC   testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC   duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC   mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC   mucosa, pancreatic duct epithelium or liver duct epithelium
CC   preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to
CC   AAY53245 represent sequences used in the exemplification of the present
CC   invention
XX
SQ   Sequence 10 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 114
AAA16552/c
ID   AAA16552 standard; DNA; 10 BP.
XX
AC   AAA16552;
```

XX
DT 16-JUN-2000 (first entry)
XX
DE Initiator consensus sequence SEQ ID NO:23.
XX
KW Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW MN/CA IX isoenzyme; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN US6027887-A.
XX
PD 22-FEB-2000.
XX
PF 24-JAN-1997; 97US-00787739.
XX
PR 21-OCT-1992; 92US-00964589.
PR 30-DEC-1993; 93US-00177093.
PR 15-JUN-1994; 94US-00260190.
PR 07-JUN-1995; 95US-00477504.
PR 07-JUN-1995; 95US-00481658.
PR 07-JUN-1995; 95US-00485049.
PR 07-JUN-1995; 95US-00485862.
PR 07-JUN-1995; 95US-00485863.
PR 07-JUN-1995; 95US-00486756.
PR 07-JUN-1995; 95US-00487077.
XX
PA (SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
XX
PI Pastorek J, Zavada J, Pastorekova S;
XX
DR WPI; 2000-194827/17.
XX
PT Nucleic acid based assay for diagnosing a wide variety of
PT preneoplastic/neoplastic disease comprises screening for the presence of
PT abnormal MN gene expression in a vertebrate.
XX
PS Disclosure; Col 85; 87pp; English.
XX
CC The present invention describes a method of screening for
CC preneoplastic/neoplastic disease. The method comprises: (1) determining
CC whether abnormal MN gene expression is present in a vertebrate; and (2)
CC if abnormal MN gene expression is determined to be present in the
CC vertebrate, determining that the vertebrate has a significant risk of
CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and
CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
CC protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC is used for detecting a wide variety of preneoplastic/neoplastic diseases
CC in a vertebrate, preferably a human. The disease detected is mammary,
CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC mucosa, pancreatic duct epithelium or liver duct epithelium
CC preneoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to
CC AAY53245 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 10 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 10 RRR 8

RESULT 115
AAA52471
ID AAA52471 standard; DNA; 10 BP.
XX
AC AAA52471;
XX
DT 25-SEP-2000 (first entry)
XX
DE Initiator (Inr) element consensus sequence.
XX
KW MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW abnormal expression; neoplastic disease; cancer; gene therapy; promoter;
KW consensus initiator element; Inr; ds.
XX
OS Unidentified.
XX
PN WO200024913-A2.
XX
PD 04-MAY-2000.
XX
PF 22-OCT-1999; 99WO-US024879.
XX
PR 23-OCT-1998; 98US-00177776.
PR 23-OCT-1998; 98US-00178115.
XX
PA (FARB) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
XX
PI Zavada J, Pastorekova S, Pastorek J;
XX
DR WPI; 2000-350752/30.
XX
PT A molecule which specifically binds to a site on MN protein (oncoprotein)
PT and prevents adhesion of vertebrate cells to the protein, useful for
PT treating preneoplastic or neoplastic diseases such as cancer.
XX
PS Disclosure; Page 27; 154pp; English.
XX
CC The invention relates to the inhibition of cell adhesion mediated by the
CC MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
CC protein). The MN protein is a tumour-associated adhesion molecule which
CC comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
CC protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
CC Abnormal expression of the MN protein is associated with tumorigenicity.
CC The invention encompasses molecules (e.g., proteins and peptides) which
CC which specifically bind to a site on the MN protein, thereby preventing
CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC also encompasses MN proteins or MN protein fragments which can be added
CC to the extracellular environment to prevent the adhesion of vertebrate
CC cells to each other. The invention also relates to the identification of
CC the binding site of the MN protein and to a method of identifying a site
CC on an MN protein to which cells adhere, comprising testing a series of
CC overlapping peptides from the protein in a cell adhesion assay. The
CC invention encompasses a vector comprising an expression control sequence
CC operatively linked to a nucleic acid encoding the variable domains of a
CC MN-specific antibody, where the domains are separated by a flexible
CC linker peptide (AAB03035) and the vector inhibits the growth of a
CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC protein. The invention also encompasses a vector comprising a nucleic
CC acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC gene promoter (AAA52473). MN proteins and peptides, MN-binding proteins
CC and peptides, and expression vectors encoding such proteins and peptides
CC are useful for treating patients with preneoplastic or neoplastic disease
CC (e.g., cancers) associated with or characterised by abnormal MN
CC expression. The present sequence represents a consensus initiator (Inr)
CC element
XX
SQ Sequence 10 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          8 YYY 10
              |||
Db          1 YYY 3
```

```
RESULT 116
AAA52471/c
ID   AAA52471 standard; DNA; 10 BP.
XX
AC   AAA52471;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Initiator (Inr) element consensus sequence.
XX
KW   MN protein; tumour associated cell adhesion molecule; oncoprotein;
KW   proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
KW   abnormal expression; neoplastic disease; cancer; gene therapy; promoter;
KW   consensus initiator element; Inr; ds.
XX
OS   Unidentified.
XX
PN   WO200024913-A2.
XX
PD   04-MAY-2000.
XX
PF   22-OCT-1999;   99WO-US024879.
XX
PR   23-OCT-1998;   98US-00177776.
PR   23-OCT-1998;   98US-00178115.
XX
PA   (FARB ) BAYER CORP.
PA   (VIRO-) INST VIROLOGY.
XX
PI   Zavada J,  Pastorekova S,  Pastorek J;
XX
DR   WPI; 2000-350752/30.
XX
PT   A molecule which specifically binds to a site on MN protein (oncoprotein)
PT   and prevents adhesion of vertebrate cells to the protein, useful for
PT   treating preneoplastic or neoplastic diseases such as cancer.
XX
PS   Disclosure; Page 27; 154pp; English.
XX
CC   The invention relates to the inhibition of cell adhesion mediated by the
CC   MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
CC   protein). The MN protein is a tumour-associated adhesion molecule which
CC   comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
CC   protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
CC   Abnormal expression of the MN protein is associated with tumorigenicity.
CC   The invention encompasses molecules (e.g., proteins and peptides) which
CC   which specifically bind to a site on the MN protein, thereby preventing
CC   adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC   also encompasses MN proteins or MN protein fragments which can be added
CC   to the extracellular environment to prevent the adhesion of vertebrate
CC   cells to each other. The invention also relates to the identification of
CC   the binding site of the MN protein and to a method of identifying a site
CC   on an MN protein to which cells adhere, comprising testing a series of
CC   overlapping peptides from the protein in a cell adhesion assay. The
CC   invention encompasses a vector comprising an expression control sequence
CC   operatively linked to a nucleic acid encoding the variable domains of a
CC   MN-specific antibody, where the domains are separated by a flexible
CC   linker peptide (AAB03035) and the vector inhibits the growth of a
CC   vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC   protein. The invention also encompasses a vector comprising a nucleic
CC   acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC   gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC   neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC   gene promoter (AAA52473). MN proteins and peptides, MN-binding proteins
CC   and peptides, and expression vectors encoding such proteins and peptides
CC   are useful for treating patients with preneoplastic or neoplastic disease
CC   (e.g., cancers) associated with or characterised by abnormal MN
CC   expression. The present sequence represents a consensus initiator (Inr)
CC   element
XX
SQ   Sequence 10 BP; 1 A; 1 C; 0 G; 0 T; 0 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          10 RRR 8
```

```
RESULT 117
AAH26710
ID   AAH26710 standard; DNA; 10 BP.
XX
AC   AAH26710;
XX
DT   26-NOV-2001  (first entry)
XX
DE   CArG box motif.
XX
KW   CArG box; smooth muscle 22 alpha; SM22-alpha; promoter; mouse;
KW   restenosis; atherosclerosis; asthma; cell proliferation; antiasthmatic;
KW   antiarteriosclerotic; gene therapy; ss.
XX
OS   Mammalia.
XX
PN   US6284743-B1.
XX
PD   04-SEP-2001.
XX
PF   10-APR-2000; 2000US-00546550.
XX
PR   05-OCT-1995;   95US-0004868P.
PR   07-OCT-1996;   96US-00726807.
PR   26-FEB-1999;   99US-00258367.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Parmacek MS,  Solway J;
XX
DR   WPI; 2001-588977/66.
XX
PT   Modulating smooth muscle cell proliferation in a mammal, useful for
PT   treating or preventing proliferation diseases, e.g. atherosclerosis,
PT   restenosis or asthma, comprises contacting cells with smooth muscle 22
PT   alpha gene promoter.
XX
PS   Example 9; Col 34; 68pp; English.
XX
CC   The present sequence is that of a CArG box motif. The motif is present in
CC   smooth muscle elements 1 and 4 of the mouse smooth muscle 22 alpha (SM22-
CC   alpha) gene promoter (see AAH26682). CArG boxes are involved in the
CC   binding of the MADS box transcription factor SRF, and may play an
CC   important role in regulating the transcription of genes encoding skeletal
CC   and cardiac alpha-actin. The invention provides methods of preventing
CC   restenosis following balloon angioplasty and methods of treating asthma.
CC   The methods are based on inhibition of smooth muscle proliferation by
CC   expressing cell cycle control genes or contraction inhibition peptides in
CC   smooth muscle cells, under the control of the SM22-alpha gene promoter
XX
SQ   Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4
```

```
RESULT 118
AAH26710/c
ID   AAH26710 standard; DNA; 10 BP.
XX
AC   AAH26710;
XX
DT   26-NOV-2001  (first entry)
XX
DE   CArG box motif.
XX
KW   CArG box; smooth muscle 22 alpha; SM22-alpha; promoter; mouse;
KW   restenosis; atherosclerosis; asthma; cell proliferation; antiasthmatic;
KW   antiarteriosclerotic; gene therapy; ss.
XX
OS   Mammalia.
XX
PN   US6284743-B1.
XX
PD   04-SEP-2001.
XX
PF   10-APR-2000; 2000US-00546550.
XX
PR   05-OCT-1995;   95US-0004868P.
PR   07-OCT-1996;   96US-00726807.
PR   26-FEB-1999;   99US-00258367.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Parmacek MS,  Solway J;
XX
DR   WPI; 2001-588977/66.
XX
PT   Modulating smooth muscle cell proliferation in a mammal, useful for
PT   treating or preventing proliferation diseases, e.g. atherosclerosis,
PT   restenosis or asthma, comprises contacting cells with smooth muscle 22
PT   alpha gene promoter.
XX
PS   Example 9; Col 34; 68pp; English.
XX
CC   The present sequence is that of a CArG box motif. The motif is present in
CC   smooth muscle elements 1 and 4 of the mouse smooth muscle 22 alpha (SM22-
CC   alpha) gene promoter (see AAH26682). CArG boxes are involved in the
CC   binding of the MADS box transcription factor SRF, and may play an
CC   important role in regulating the transcription of genes encoding skeletal
CC   and cardiac alpha-actin. The invention provides methods of preventing
CC   restenosis following balloon angioplasty and methods of treating asthma.
CC   The methods are based on inhibition of smooth muscle proliferation by
CC   expressing cell cycle control genes or contraction inhibition peptides in
CC   smooth muscle cells, under the control of the SM22-alpha gene promoter
XX
SQ   Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          4 WWG 2


RESULT 119
AAD20602
ID   AAD20602 standard; DNA; 10 BP.
XX
AC   AAD20602;
XX
DT   03-JAN-2002  (first entry)
XX
DE   Consensus CArG box embedded in a smooth muscle element.
XX
KW   Murine; SM22alpha; therapy; restenosis; balloon angioplasty; asthma;
KW   smooth muscle cell; proliferation; vasotropic; smooth muscle element;
KW   SME; ds.
XX
OS   Mus musculus.
OS   Unidentified.
XX
PN   US6291211-B1.
XX
PD   18-SEP-2001.
XX
PF   01-NOV-1999;   99US-00431414.
XX
PR   05-OCT-1995;   95US-0004868P.
PR   07-OCT-1996;   96US-00726807.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Parmacek MS,  Solway J;
XX
DR   WPI; 2001-637950/73.
XX
PT   Expressing a polypeptide other than a mouse SM22alpha in a cell, useful
PT   in treating restenosis, by providing to the cell a nucleic acid construct
PT   comprising an SM22alpha promoter operably linked to the sequence encoding
PT   the polypeptide.
XX
PS   Example 9; Col 33; 68pp; English.
XX
CC   The present invention relates to a method for expressing a polypeptide
CC   other than a mouse SM22alpha in a cell comprising providing to the cell a
CC   nucleic acid construct having an SM22alpha promoter operably linked to a
CC   nucleotide sequence encoding the polypeptide. The method is useful for
CC   preventing restenosis following balloon angioplasty and treating asthma
CC   based on inhibition of smooth muscle cell proliferation by expressing
CC   cell cycle control genes. The present sequence is a consensus CArG box
CC   embedded in a smooth muscle element (SME)
XX
SQ   Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 120
AAD20602/c
ID   AAD20602 standard; DNA; 10 BP.
XX
AC   AAD20602;
XX
DT   03-JAN-2002  (first entry)
XX
DE   Consensus CArG box embedded in a smooth muscle element.
XX
KW   Murine; SM22alpha; therapy; restenosis; balloon angioplasty; asthma;
KW   smooth muscle cell; proliferation; vasotropic; smooth muscle element;
KW   SME; ds.
XX
OS   Mus musculus.
OS   Unidentified.
XX
PN   US6291211-B1.
XX
PD   18-SEP-2001.
XX
PF   01-NOV-1999;   99US-00431414.
XX
PR   05-OCT-1995;   95US-0004868P.
```

PR 07-OCT-1996; 96US-00726807.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Parmacek MS, Solway J;
XX
DR WPI; 2001-637950/73.
XX
PT Expressing a polypeptide other than a mouse SM22alpha in a cell, useful
PT in treating restenosis, by providing to the cell a nucleic acid construct
PT comprising an SM22alpha promoter operably linked to the sequence encoding
PT the polypeptide.
XX
PS Example 9; Col 33; 68pp; English.
XX
CC The present invention relates to a method for expressing a polypeptide
CC other than a mouse SM22alpha in a cell comprising providing to the cell a
CC nucleic acid construct having an SM22alpha promoter operably linked to a
CC nucleotide sequence encoding the polypeptide. The method is useful for
CC preventing restenosis following balloon angioplasty and treating asthma
CC based on inhibition of smooth muscle cell proliferation by expressing
CC cell cycle control genes. The present sequence is a consensus CArG box
CC embedded in a smooth muscle element (SME)
XX
SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
|||
Db 9 CWW 7

RESULT 121
AAD21142
ID AAD21142 standard; DNA; 10 BP.
XX
AC AAD21142;
XX
DT 15-JAN-2002 (first entry)
XX
DE Consensus CArG box embedded in smooth muscle element (SME).
XX
KW Murine; vasotropic; cytostatic; angiogenesis; smooth muscle cell; SMC;
KW SM22 alpha; atherosclerosis; arterial injury; balloon angioplasty;
KW restenosis; airway blockage; asthma; proliferative disease; SME;
KW smooth muscle element; ds.
XX
OS Mus musculus.
XX
PN US6297221-B1.
XX
PD 02-OCT-2001.
XX
PF 05-JAN-1999; 99US-00225670.
XX
PR 05-OCT-1995; 95US-0004868P.
PR 07-OCT-1996; 96US-00726807.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Parmacek MS, Solway J;
XX
DR WPI; 2001-647294/74.
XX
PT Promoting angiogenesis and preventing atherosclerosis or restenosis
PT following balloon angioplasty, comprises providing to smooth muscle cell
PT nucleic acid construct containing an SM22 alpha promoter.
XX
PS Example 9; Col 33; 67pp; English.
XX
CC The patent discloses a method for promoting angiogenesis in a mammal by
CC providing a nucleic acid construct comprising an SM22 alpha promoter to a
CC smooth muscle cell (SMC) in the mammal. The promoter is operably linked
CC to a nucleotide sequence encoding a polypeptide or RNA competent to
CC induce angiogenesis. The method is useful for promoting angiogenesis, for
CC preventing atherosclerosis, restenosis or other arterial injury following
CC balloon angioplasty and airway blockage in asthma. The promoter may be
CC used to express heterologous proteins or mRNAs in proliferating smooth
CC muscle cells and to control proliferative diseases, or to promote
CC angiogenesis. The present sequence is a consensus CArG box embedded in
CC nuclear protein binding sites, designated as smooth muscle element (SME).
CC This sequence binds to the MADS box transcription factor, SRF and play an
CC important role in regulating the transcription of genes encoding skeletal
CC and cardiac alpha actin
XX
SQ Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
|||
Db 2 CWW 4

RESULT 122
AAD21142/c
ID AAD21142 standard; DNA; 10 BP.
XX
AC AAD21142;
XX
DT 15-JAN-2002 (first entry)
XX
DE Consensus CArG box embedded in smooth muscle element (SME).
XX
KW Murine; vasotropic; cytostatic; angiogenesis; smooth muscle cell; SMC;
KW SM22 alpha; atherosclerosis; arterial injury; balloon angioplasty;
KW restenosis; airway blockage; asthma; proliferative disease; SME;
KW smooth muscle element; ds.
XX
OS Mus musculus.
XX
PN US6297221-B1.
XX
PD 02-OCT-2001.
XX
PF 05-JAN-1999; 99US-00225670.
XX
PR 05-OCT-1995; 95US-0004868P.
PR 07-OCT-1996; 96US-00726807.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Parmacek MS, Solway J;
XX
DR WPI; 2001-647294/74.
XX
PT Promoting angiogenesis and preventing atherosclerosis or restenosis
PT following balloon angioplasty, comprises providing to smooth muscle cell
PT nucleic acid construct containing an SM22 alpha promoter.
XX
PS Example 9; Col 33; 67pp; English.
XX
CC The patent discloses a method for promoting angiogenesis in a mammal by
CC providing a nucleic acid construct comprising an SM22 alpha promoter to a
CC smooth muscle cell (SMC) in the mammal. The promoter is operably linked
CC to a nucleotide sequence encoding a polypeptide or RNA competent to
CC induce angiogenesis. The method is useful for promoting angiogenesis, for
CC preventing atherosclerosis, restenosis or other arterial injury following
CC balloon angioplasty and airway blockage in asthma. The promoter may be
CC used to express heterologous proteins or mRNAs in proliferating smooth
CC muscle cells and to control proliferative diseases, or to promote

```
CC   angiogenesis. The present sequence is a consensus CArG box embedded in
CC   nuclear protein binding sites, designated as smooth muscle element (SME).
CC   This sequence binds to the MADS box transcription factor, SRF and play an
CC   important role in regulating the transcription of genes encoding skeletal
CC   and cardiac alpha actin
XX
SQ   Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          4 WWG 2


RESULT 123
AAD04664
ID   AAD04664 standard; DNA; 10 BP.
XX
AC   AAD04664;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Thermus 9kb SphI fragment consensus direct repeat I of pTsp45L plasmid.
XX
KW   Replication protein; RepT; partition protein; ParA; pTsp45S plasmid;
KW   kanamycin-resistance gene; thermophilic transformation; Ori;
KW   replication origin; ds.
XX
OS   Thermus sp.
XX
PN   US6207377-B1.
XX
PD   27-MAR-2001.
XX
PF   14-AUG-1998;   98US-00134246.
XX
PR   14-AUG-1998;   98US-00134246.
XX
PA   (NEWE ) NEW ENGLAND BIOLABS INC.
XX
PI   Wayne J,  Xu S;
XX
DR   WPI; 2001-298939/31.
XX
PT   Cloning Thermus species (Ts) plasmid genes comprises transforming
PT   Escherichia coli with cloned recombinant plasmid containing Ts and E.coli
PT   origins of replication, isolating cloned recombinant plasmid from E.coli
PT   and transforming Ts cell.
XX
PS   Example II; Col 8; 32pp; English.
XX
CC   The present DNA sequence is Thermus 9kb SphI fragment consensus direct
CC   repeat I of pTsp45L plasmid. This 9kb SphI fragment encodes a partition
CC   protein, parA gene. The direct repeat is important for pTsp45L plasmid
CC   replication. The invention relates to Thermus sp. replication protein
CC   RepT, partition protein ParA and their corresponding DNA molecules which
CC   relates to recombinant DNA molecules encoding plasmid DNA replication
CC   origins in Thermus, as well as to shuttle vectors which contain the same.
CC   The invention also relates to method useful for cloning Thermus sp.
CC   plasmid genes which comprises inserting plasmid DNA comprising a Thermus
CC   sp. origin of replication (Ori) into a recombinant plasmid comprising a
CC   thermostable kanamycin-resistance gene and an Escherichia coli Ori, to
CC   produce a cloned recombinant plasmid. This cloned recombinant plasmid is
CC   transformed with an E. coli. host cell, and E. coli. host cell cultured
CC   for the expression of cloned recombinant plasmid. The cloned recombinant
CC   plasmid isolated from E. coli host cell is then transformed with Thermus
CC   sp. host cell and Thermus sp. host cell is cultured. Thus Thermus sp.
CC   plasmid genes are cloned. These plasmid DNAs are used for thermophilic
CC   transformation
XX
SQ   Sequence 10 BP; 0 A; 1 C; 0 G; 4 T; 0 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 5;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          1 RRC 3


RESULT 124
AAD04664/c
ID   AAD04664 standard; DNA; 10 BP.
XX
AC   AAD04664;
XX
DT   04-JUL-2001  (first entry)
XX
DE   Thermus 9kb SphI fragment consensus direct repeat I of pTsp45L plasmid.
XX
KW   Replication protein; RepT; partition protein; ParA; pTsp45S plasmid;
KW   kanamycin-resistance gene; thermophilic transformation; Ori;
KW   replication origin; ds.
XX
OS   Thermus sp.
XX
PN   US6207377-B1.
XX
PD   27-MAR-2001.
XX
PF   14-AUG-1998;   98US-00134246.
XX
PR   14-AUG-1998;   98US-00134246.
XX
PA   (NEWE ) NEW ENGLAND BIOLABS INC.
XX
PI   Wayne J,  Xu S;
XX
DR   WPI; 2001-298939/31.
XX
PT   Cloning Thermus species (Ts) plasmid genes comprises transforming
PT   Escherichia coli with cloned recombinant plasmid containing Ts and E.coli
PT   origins of replication, isolating cloned recombinant plasmid from E.coli
PT   and transforming Ts cell.
XX
PS   Example II; Col 8; 32pp; English.
XX
CC   The present DNA sequence is Thermus 9kb SphI fragment consensus direct
CC   repeat I of pTsp45L plasmid. This 9kb SphI fragment encodes a partition
CC   protein, parA gene. The direct repeat is important for pTsp45L plasmid
CC   replication. The invention relates to Thermus sp. replication protein
CC   RepT, partition protein ParA and their corresponding DNA molecules which
CC   relates to recombinant DNA molecules encoding plasmid DNA replication
CC   origins in Thermus, as well as to shuttle vectors which contain the same.
CC   The invention also relates to method useful for cloning Thermus sp.
CC   plasmid genes which comprises inserting plasmid DNA comprising a Thermus
CC   sp. origin of replication (Ori) into a recombinant plasmid comprising a
CC   thermostable kanamycin-resistance gene and an Escherichia coli Ori, to
CC   produce a cloned recombinant plasmid. This cloned recombinant plasmid is
CC   transformed with an E. coli. host cell, and E. coli. host cell cultured
CC   for the expression of cloned recombinant plasmid. The cloned recombinant
CC   plasmid isolated from E. coli host cell is then transformed with Thermus
CC   sp. host cell and Thermus sp. host cell is cultured. Thus Thermus sp.
CC   plasmid genes are cloned. These plasmid DNAs are used for thermophilic
CC   transformation
XX
SQ   Sequence 10 BP; 0 A; 1 C; 0 G; 4 T; 0 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 5;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 RRR 3
              |||
Db         10 RRR 8
```

RESULT 125
ABK33367
ID ABK33367 standard; DNA; 10 BP.
XX
AC ABK33367;
XX
DT 08-MAY-2002 (first entry)
XX
DE SRF binding site or CArG box.
XX
KW SM22alpha; smooth muscle cell specific protein; ds; vasotropic;
KW antiasthmatic; muscular; bioprosthesis; EMSA; gene therapy;
KW electrophoretic mobility shift assay; restenosis; balloon angioplasty;
KW arterial injury; angiogenesis; graft; stent implant; asthma;
KW smooth muscle cell proliferative disease;
KW transcription factor binding site.
XX
OS Mammalia.
XX
PN US6331527-B1.
XX
PD 18-DEC-2001.
XX
PF 01-NOV-1999; 99US-00431349.
XX
PR 05-OCT-1995; 95US-0004868P.
PR 07-OCT-1996; 96US-00726807.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Parmacek MS, Solway J;
XX
DR WPI; 2002-129550/17.
XX
PT A bioprothesis for use in the prevention of restenosis and in the
PT prevention and treatment of smooth muscle cell proliferative diseases
PT comprises a smooth muscle cell transfected with an SM22-alpha promoter
PT operably linked to a DNA sequence.
XX
PS Example 9; Col 33; 69pp; English.
XX
CC The invention relates to a bioprosthesis comprises a smooth muscle cell
CC transfected with a nucleic acid segment comprising an SM22alpha promoter
CC region operably linked to a DNA sequence encoding a molecule other than
CC mouse SM22alpha (a smooth muscle specific protein). Also included are a
CC method of providing a molecule of interest to a blood vessel in a mammal
CC by providing a bioprosthesis comprising, placing in a blood vessel and
CC obtaining expression and a method of providing a molecule of interest to
CC a blood vessel in a mammal by providing a bioprosthesis comprising an
CC oligomer comprising SME1 - SME6, corresponding to the EMSA
CC (electrophoretic mobility shift assay) appearing as ABK33341, ABK33343,
CC ABK33345, ABK33347 ABK33351 and ABK33353 or a sequence that hybridizes
CC with the complement of the above sequences, placing in a blood vessel and
CC obtaining expression. The bioprosthesis can be used in methods to provide
CC a molecule of interest to a blood vessel in a mammal (i.e by gene
CC therapy). It can also be used in the prevention of restenosis following
CC balloon angioplasty or other arterial injury, in the promotion of
CC angiogenesis in graft or stent implants and in the treatment or
CC prevention of asthma along with other smooth muscle cell proliferative
CC diseases. The control of expression of the smooth muscle cell specific
CC promoter is constitutive and cell cycle independent, it thus promotes
CC transcription in both resting and proliferating cells in contrast to
CC other known smooth muscle cell promoters that are down regulated in
CC proliferating cells. The present sequence is a transcription factor
CC binding site sequence found in SM22alpha or related genes
XX
SQ Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;

```
  Query Match           30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4
```

RESULT 126
ABK33367/c
ID ABK33367 standard; DNA; 10 BP.
XX
AC ABK33367;
XX
DT 08-MAY-2002 (first entry)
XX
DE SRF binding site or CArG box.
XX
KW SM22alpha; smooth muscle cell specific protein; ds; vasotropic;
KW antiasthmatic; muscular; bioprosthesis; EMSA; gene therapy;
KW electrophoretic mobility shift assay; restenosis; balloon angioplasty;
KW arterial injury; angiogenesis; graft; stent implant; asthma;
KW smooth muscle cell proliferative disease;
KW transcription factor binding site.
XX
OS Mammalia.
XX
PN US6331527-B1.
XX
PD 18-DEC-2001.
XX
PF 01-NOV-1999; 99US-00431349.
XX
PR 05-OCT-1995; 95US-0004868P.
PR 07-OCT-1996; 96US-00726807.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Parmacek MS, Solway J;
XX
DR WPI; 2002-129550/17.
XX
PT A bioprothesis for use in the prevention of restenosis and in the
PT prevention and treatment of smooth muscle cell proliferative diseases
PT comprises a smooth muscle cell transfected with an SM22-alpha promoter
PT operably linked to a DNA sequence.
XX
PS Example 9; Col 33; 69pp; English.
XX
CC The invention relates to a bioprosthesis comprises a smooth muscle cell
CC transfected with a nucleic acid segment comprising an SM22alpha promoter
CC region operably linked to a DNA sequence encoding a molecule other than
CC mouse SM22alpha (a smooth muscle specific protein). Also included are a
CC method of providing a molecule of interest to a blood vessel in a mammal
CC by providing a bioprosthesis comprising, placing in a blood vessel and
CC obtaining expression and a method of providing a molecule of interest to
CC a blood vessel in a mammal by providing a bioprosthesis comprising an
CC oligomer comprising SME1 - SME6, corresponding to the EMSA
CC (electrophoretic mobility shift assay) appearing as ABK33341, ABK33343,
CC ABK33345, ABK33347 ABK33351 and ABK33353 or a sequence that hybridizes
CC with the complement of the above sequences, placing in a blood vessel and
CC obtaining expression. The bioprosthesis can be used in methods to provide
CC a molecule of interest to a blood vessel in a mammal (i.e by gene
CC therapy). It can also be used in the prevention of restenosis following
CC balloon angioplasty or other arterial injury, in the promotion of
CC angiogenesis in graft or stent implants and in the treatment or
CC prevention of asthma along with other smooth muscle cell proliferative
CC diseases. The control of expression of the smooth muscle cell specific
CC promoter is constitutive and cell cycle independent, it thus promotes
CC transcription in both resting and proliferating cells in contrast to
CC other known smooth muscle cell promoters that are down regulated in
CC proliferating cells. The present sequence is a transcription factor

```
CC   binding site sequence found in SM22alpha or related genes
XX
SQ   Sequence 10 BP; 0 A; 4 C; 0 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          4 WWG 2


RESULT 127
ABK85627
ID   ABK85627 standard; DNA; 10 BP.
XX
AC   ABK85627;
XX
DT   16-AUG-2002  (first entry)
XX
DE   Serum responsive element (SRE) consensus sequence.
XX
KW   NET; ss; ERP; SAP-1; angiogenesis; transgenic; ulcer; SRE; gel-shift;
KW   ischaemia; wound healing; vascular restenosis; hypertension; dementia;
KW   alzheimer's disease; lymphoedema; atherosclerosis; haemangioma; bone;
KW   haemangioendothelioma; ovarian hyperstimulation; endometriosis; ascites;
KW   follicular cyst; Kaposi sarcoma; tumour; cancer; allergy; synovitis;
KW   respiratory distress; rheumatoid arthritis; pneumonia; thyroiditis;
KW   cartilage dysfunction; obesity; asthma; inflammation; hepatitis;
KW   glomerulonephritis; diabetic retinopathy; thyroiditis; nasal polyp;
KW   serum response element.
XX
OS   Unidentified.
XX
PN   EP1202065-A1.
XX
PD   02-MAY-2002.
XX
PF   25-OCT-2000; 2000EP-00402968.
XX
PR   25-OCT-2000; 2000EP-00402968.
XX
PA   (AVET ) AVENTIS PHARMA SA.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   Wasylyk B,  Multon M,  Ayadi A,  Zheng H;
XX
DR   WPI; 2002-437317/47.
XX
PT   Use of all or part of a NET polypeptide to identify compounds useful to
PT   modulate angiogenesis and prevent or treat pathologies associated with
PT   angiogenic disorders e.g. cardiac ischemia, atherosclerosis or tumor
PT   growth.
XX
PS   Disclosure; Page 2; 77pp; English.
XX
CC   This invention relates to the use of all or part of a NET (also known as
CC   ERP or SAP-1) polypeptide to identify compounds modulating angiogenesis
CC   or compounds that can be used to prevent or treat pathologies associated
CC   with angiogenic disorders. The invention also comprises transgenic
CC   animals that bear mutations in the NET gene. The method and transgenic
CC   animals of the invention are useful to identify compounds to treat
CC   pathologies associated with angiogenic disorders involving insufficient
CC   vascularisation and requiring increased angiogenesis (e.g. cardiac/
CC   peripheral ischaemia, defects in wound healing and vascular restenosis,
CC   hypertension, ulcers, alzheimer's disease, lymphooedema, dementia) or
CC   involving increased vascularisation and requiring decreased angiogenesis
CC   (e.g. atherosclerosis, haemangioma, haemangioendothelioma, ovarian
CC   hyperstimulation, endometriosis, ascites, follicular cysts, ). They are
CC   also useful to identify compounds useful to treat pathologies associated
CC   with angiogenic disorders such as Kaposi sarcoma, tumour growth and
CC   cancer, or other pathologies in which NET is activated). Such compounds
CC   may also be used to treat allergies, dysfunctional uterine bleeding,
CC   respiratory distress, rheumatoid arthritis, bone and cartilage
CC   dysfunction, obesity, synovitis, inflammation, hepatitis,
CC   glomerulonephritis, asthma, retinopathy, thyroiditis, pneumonia, nasal
CC   polyps and thyroiditis. Such compounds may be e.g. antisense
CC   polynucleotides downregulating or blocking expression of a NET gene,
CC   intracellular binding proteins or NET dominant negative mutants.
CC   Compounds modulating NET activity may also be included in medicaments to
CC   prevent and/or treat pathologies associated with angiogenic disorders.
CC   The present sequence represents a serum responsive element (SRE)
CC   consensus sequence shown in the specification
XX
SQ   Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          2 CWW 4


RESULT 128
ABK85627/c
ID   ABK85627 standard; DNA; 10 BP.
XX
AC   ABK85627;
XX
DT   16-AUG-2002  (first entry)
XX
DE   Serum responsive element (SRE) consensus sequence.
XX
KW   NET; ss; ERP; SAP-1; angiogenesis; transgenic; ulcer; SRE; gel-shift;
KW   ischaemia; wound healing; vascular restenosis; hypertension; dementia;
KW   alzheimer's disease; lymphoedema; atherosclerosis; haemangioma; bone;
KW   haemangioendothelioma; ovarian hyperstimulation; endometriosis; ascites;
KW   follicular cyst; Kaposi sarcoma; tumour; cancer; allergy; synovitis;
KW   respiratory distress; rheumatoid arthritis; pneumonia; thyroiditis;
KW   cartilage dysfunction; obesity; asthma; inflammation; hepatitis;
KW   glomerulonephritis; diabetic retinopathy; thyroiditis; nasal polyp;
KW   serum response element.
XX
OS   Unidentified.
XX
PN   EP1202065-A1.
XX
PD   02-MAY-2002.
XX
PF   25-OCT-2000; 2000EP-00402968.
XX
PR   25-OCT-2000; 2000EP-00402968.
XX
PA   (AVET ) AVENTIS PHARMA SA.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI   Wasylyk B,  Multon M,  Ayadi A,  Zheng H;
XX
DR   WPI; 2002-437317/47.
XX
PT   Use of all or part of a NET polypeptide to identify compounds useful to
PT   modulate angiogenesis and prevent or treat pathologies associated with
PT   angiogenic disorders e.g. cardiac ischemia, atherosclerosis or tumor
PT   growth.
XX
PS   Disclosure; Page 2; 77pp; English.
XX
CC   This invention relates to the use of all or part of a NET (also known as
CC   ERP or SAP-1) polypeptide to identify compounds modulating angiogenesis
CC   or compounds that can be used to prevent or treat pathologies associated
CC   with angiogenic disorders. The invention also comprises transgenic
CC   animals that bear mutations in the NET gene. The method and transgenic
CC   animals of the invention are useful to identify compounds to treat
```

```
CC   pathologies associated with angiogenic disorders involving insufficient
CC   vascularisation and requiring increased angiogenesis (e.g. cardiac/
CC   peripheral ischaemia, defects in wound healing and vascular restenosis,
CC   hypertension, ulcers, alzheimer's disease, lymphooedema, dementia) or
CC   involving increased vascularisation and requiring decreased angiogenesis
CC   (e.g. atherosclerosis, haemangioma, haemangioendothelioma, ovarian
CC   hyperstimulation, endometriosis, ascites, follicular cysts, ). They are
CC   also useful to identify compounds useful to treat pathologies associated
CC   with angiogenic disorders such as Kaposi sarcoma, tumour growth and
CC   cancer, or other pathologies in which NET is activated). Such compounds
CC   may also be used to treat allergies, dysfunctional uterine bleeding,
CC   respiratory distress, rheumatoid arthritis, bone and cartilage
CC   dysfunction, obesity, synovitis, inflammation, hepatitis,
CC   glomerulonephritis, asthma, retinopathy, thyroiditis, pneumonia, nasal
CC   polyps and thyroiditis. Such compounds may be e.g. antisense
CC   polynucleotides downregulating or blocking expression of a NET gene,
CC   intracellular binding proteins or NET dominant negative mutants.
CC   Compounds modulating NET activity may also be included in medicaments to
CC   prevent and/or treat pathologies associated with angiogenic disorders.
CC   The present sequence represents a serum responsive element (SRE)
CC   consensus sequence shown in the specification
XX
SQ   Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7


RESULT 129
ABL53549
ID   ABL53549 standard; DNA; 10 BP.
XX
AC   ABL53549;
XX
DT   10-JUN-2002  (first entry)
XX
DE   CpG motif.
XX
KW   CpG; autoimmune disease; insulin dependent diabetes mellitus; IDDM;
KW   DNA immunisation; vaccine; antidiabetic; immunotherapy; gene therapy; ss.
XX
OS   Synthetic.
XX
PN   WO200216549-A2.
XX
PD   28-FEB-2002.
XX
PF   23-AUG-2001; 2001WO-IL000790.
XX
PR   25-AUG-2000; 2000US-0227853P.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Cohen IR,  Quintana FJ;
XX
DR   WPI; 2002-227369/28.
XX
PT   Treating or preventing an ongoing autoimmune disease e.g. diabetes,
PT   comprises vaccination with a DNA sequence comprising a CpG motif.
XX
PS   Disclosure; Page 9; 53pp; English.
XX
CC   The present sequence is that of an example of a CpG motif. The invention
CC   relates to methods for the prevention or treatment of autoimmune disease,
CC   particularly insulin dependent diabetes mellitus (IDDM). A DNA vaccine
CC   which includes a CpG motif, such as that given in the CpG oligonucleotide
CC   of ABL53541, is preferably used. The vaccine may also include DNA
CC   encoding an antigen associated with the autoimmune disease
XX
SQ   Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          1 RRC 3


RESULT 130
ABL53549/c
ID   ABL53549 standard; DNA; 10 BP.
XX
AC   ABL53549;
XX
DT   10-JUN-2002  (first entry)
XX
DE   CpG motif.
XX
KW   CpG; autoimmune disease; insulin dependent diabetes mellitus; IDDM;
KW   DNA immunisation; vaccine; antidiabetic; immunotherapy; gene therapy; ss.
XX
OS   Synthetic.
XX
PN   WO200216549-A2.
XX
PD   28-FEB-2002.
XX
PF   23-AUG-2001; 2001WO-IL000790.
XX
PR   25-AUG-2000; 2000US-0227853P.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Cohen IR,  Quintana FJ;
XX
DR   WPI; 2002-227369/28.
XX
PT   Treating or preventing an ongoing autoimmune disease e.g. diabetes,
PT   comprises vaccination with a DNA sequence comprising a CpG motif.
XX
PS   Disclosure; Page 9; 53pp; English.
XX
CC   The present sequence is that of an example of a CpG motif. The invention
CC   relates to methods for the prevention or treatment of autoimmune disease,
CC   particularly insulin dependent diabetes mellitus (IDDM). A DNA vaccine
CC   which includes a CpG motif, such as that given in the CpG oligonucleotide
CC   of ABL53541, is preferably used. The vaccine may also include DNA
CC   encoding an antigen associated with the autoimmune disease
XX
SQ   Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db         10 RRC 8


RESULT 131
ADG88268
ID   ADG88268 standard; DNA; 10 BP.
XX
AC   ADG88268;
XX
DT   22-APR-2004  (first entry)
XX
DE   Pathogen infection-related gene consensus motif 1 cis element #710.
```

```
XX
KW   Pathogen infection-related gene; plant; Peronospora parasitica;
KW   defence mechanism; pathogen resistance; transgenic plant; oomycete;
KW   fungus; bacterium; virus; nematode; insect; aphid; promoter; cis element;
KW   motif 1; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200222675-A2.
XX
PD   21-MAR-2002.
XX
PF   14-SEP-2001; 2001WO-US028506.
XX
PR   15-SEP-2000; 2000US-0232778P.
PR   22-JUN-2001; 2001US-0300183P.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA   (UYNC-) UNIV NORTH CAROLINA.
PA   (GLAZ/) GLAZEBROOK J.
PA   (WANG/) WANG X.
PA   (DANG/) DANGL J L.
PA   (EULG/) EULGEM T.
PA   (ZHUT/) ZHU T.
XX
PI   Glazebrook J,  Wang X,  Dangl JL,  Eulgem T,  Zhu T;
XX
DR   WPI; 2002-292409/33.
XX
PT   Novel isolated polynucleotide, useful for conveying pathogen resistance
PT   to plants, and for identifying plants infected with a pathogen.
XX
PS   Claim 44; SEQ ID NO 710; 605pp; English.
XX
CC   The invention relates to 691 Arabidopsis thaliana genes (ADG87559--
CC   ADG87557}) whose expression is altered in response to pathogen infection,
CC   and to homologues of these genes from other plants or fungi, especially
CC   from maize, soybean, barley, alfalfa, sunflower, canola (oilseed rape),
CC   cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The
CC   expression of genes of the invention was upregulated or downregulated in
CC   Arabidopsis plants infected with the oomycete Peronospora parasitica,
CC   indicating that they play a role in defence mechanisms. The genes of the
CC   invention are regulated by RPP7 or RRP8 which act via unconventional
CC   signalling cascades, or by the RPP4-dependent pathway. The invention also
CC   relates to polypeptides encoded by the pathogen infection-related genes;
CC   promoter motifs from pathogen infection-related genes (ADG88243-ADG88327)
CC   ; expression cassettes, host cells and pathogen-resistant transgenic
CC   plants and their progeny comprising a polynucleotide of the invention;
CC   and a method of identifying a plant cell infected with a pathogen. The
CC   polynucleotide sequences and methods of the invention are useful for
CC   identifying plants infected with a pathogen, and for conferring
CC   resistance to pathogens such as oomycetes, fungi, bacteria, viruses,
CC   neamotodes and insects (e.g., aphids). The present sequence represents a
CC   consensus sequence for cis elements from the promoters of Arabidopsis
CC   thaliana genes whose expression is altered in response to Peronospora
CC   parasitica infection. Note: The sequence data for this patent can also be
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 1 G; 1 T; 0 U; 4 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          4 CWW 6


RESULT 132
ADG88268/c
ID   ADG88268 standard; DNA; 10 BP.
XX
AC   ADG88268;
XX
DT   22-APR-2004  (first entry)
XX
DE   Pathogen infection-related gene consensus motif 1 cis element #710.
XX
KW   Pathogen infection-related gene; plant; Peronospora parasitica;
KW   defence mechanism; pathogen resistance; transgenic plant; oomycete;
KW   fungus; bacterium; virus; nematode; insect; aphid; promoter; cis element;
KW   motif 1; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200222675-A2.
XX
PD   21-MAR-2002.
XX
PF   14-SEP-2001; 2001WO-US028506.
XX
PR   15-SEP-2000; 2000US-0232778P.
PR   22-JUN-2001; 2001US-0300183P.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA   (UYNC-) UNIV NORTH CAROLINA.
PA   (GLAZ/) GLAZEBROOK J.
PA   (WANG/) WANG X.
PA   (DANG/) DANGL J L.
PA   (EULG/) EULGEM T.
PA   (ZHUT/) ZHU T.
XX
PI   Glazebrook J,  Wang X,  Dangl JL,  Eulgem T,  Zhu T;
XX
DR   WPI; 2002-292409/33.
XX
PT   Novel isolated polynucleotide, useful for conveying pathogen resistance
PT   to plants, and for identifying plants infected with a pathogen.
XX
PS   Claim 44; SEQ ID NO 710; 605pp; English.
XX
CC   The invention relates to 691 Arabidopsis thaliana genes (ADG87559--
CC   ADG87557}) whose expression is altered in response to pathogen infection,
CC   and to homologues of these genes from other plants or fungi, especially
CC   from maize, soybean, barley, alfalfa, sunflower, canola (oilseed rape),
CC   cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The
CC   expression of genes of the invention was upregulated or downregulated in
CC   Arabidopsis plants infected with the oomycete Peronospora parasitica,
CC   indicating that they play a role in defence mechanisms. The genes of the
CC   invention are regulated by RPP7 or RRP8 which act via unconventional
CC   signalling cascades, or by the RPP4-dependent pathway. The invention also
CC   relates to polypeptides encoded by the pathogen infection-related genes;
CC   promoter motifs from pathogen infection-related genes (ADG88243-ADG88327)
CC   ; expression cassettes, host cells and pathogen-resistant transgenic
CC   plants and their progeny comprising a polynucleotide of the invention;
CC   and a method of identifying a plant cell infected with a pathogen. The
CC   polynucleotide sequences and methods of the invention are useful for
CC   identifying plants infected with a pathogen, and for conferring
CC   resistance to pathogens such as oomycetes, fungi, bacteria, viruses,
CC   neamotodes and insects (e.g., aphids). The present sequence represents a
CC   consensus sequence for cis elements from the promoters of Arabidopsis
CC   thaliana genes whose expression is altered in response to Peronospora
CC   parasitica infection. Note: The sequence data for this patent can also be
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 10 BP; 2 A; 2 C; 1 G; 1 T; 0 U; 4 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
```

```
Db          6 WWG 4


RESULT 133
ABZ24785
ID   ABZ24785 standard; DNA; 10 BP.
XX
AC   ABZ24785;
XX
DT   07-APR-2003  (first entry)
XX
DE   Oligodeoxynucleic acid molecule ODN 16-A.
XX
KW   Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .10
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "thiophosphate backbone"
XX
PN   WO200295027-A2.
XX
PD   28-NOV-2002.
XX
PF   17-MAY-2002; 2002WO-EP005448.
XX
PR   21-MAY-2001; 2001AT-00000805.
XX
PA   (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI   Lingnau K,  Schellack C,  Schmidt W;
XX
DR   WPI; 2003-183880/18.
XX
PT   New oligodeoxynucleic acid molecules useful for the preparation of
PT   vaccine.
XX
PS   Example 9; Page 35; 57pp; English.
XX
CC   The present sequence is that of a thiosubstituted oligodeoxynucleic acid
CC   molecule, ODN 16-A, including a deoxyuridine monophosphate. The invention
CC   is based on the discovery that ODNs containing deoxyuridine residues (U-
CC   ODNs) have an immunostimulatory effect comparable to, or in many
CC   instances greater than, ODNs containing CpG motifs, producing higher
CC   numbers of specific T cells to a given antigen. The U-ODNs do not induce
CC   the systemic production of pro-inflammatory cytokines and, in contrast to
CC   CpG ODNs, are not dependent on a specific motif or a palindromic
CC   sequence. Use of a U-ODN for the preparation of a vaccine is claimed.
CC   Combining the U-ODN with an antigen strongly increases the potential of
CC   the antigen to raise the protection/immune response of a vaccinated
CC   individual. An example of the invention demonstrated the generation of a
CC   specific immune response against a melanoma-derived peptide (see
CC   ABP58360) by injection of mice with the peptide in combination with ODN
CC   16-A
XX
SQ   Sequence 10 BP; 0 A; 0 C; 0 G; 1 T; 1 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 8;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 134
ABZ24785/c
ID   ABZ24785 standard; DNA; 10 BP.
XX
AC   ABZ24785;
XX
DT   07-APR-2003  (first entry)
XX
DE   Oligodeoxynucleic acid molecule ODN 16-A.
XX
KW   Immunostimulant; oligodeoxynucleic acid; ODN; vaccine; DNA-RNA hybrid;
KW   ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .10
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "thiophosphate backbone"
XX
PN   WO200295027-A2.
XX
PD   28-NOV-2002.
XX
PF   17-MAY-2002; 2002WO-EP005448.
XX
PR   21-MAY-2001; 2001AT-00000805.
XX
PA   (INTE-) INTERCELL BIOMEDIZINISCHE FORSCHUNGS.
PA   (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI   Lingnau K,  Schellack C,  Schmidt W;
XX
DR   WPI; 2003-183880/18.
XX
PT   New oligodeoxynucleic acid molecules useful for the preparation of
PT   vaccine.
XX
PS   Example 9; Page 35; 57pp; English.
XX
CC   The present sequence is that of a thiosubstituted oligodeoxynucleic acid
CC   molecule, ODN 16-A, including a deoxyuridine monophosphate. The invention
CC   is based on the discovery that ODNs containing deoxyuridine residues (U-
CC   ODNs) have an immunostimulatory effect comparable to, or in many
CC   instances greater than, ODNs containing CpG motifs, producing higher
CC   numbers of specific T cells to a given antigen. The U-ODNs do not induce
CC   the systemic production of pro-inflammatory cytokines and, in contrast to
CC   CpG ODNs, are not dependent on a specific motif or a palindromic
CC   sequence. Use of a U-ODN for the preparation of a vaccine is claimed.
CC   Combining the U-ODN with an antigen strongly increases the potential of
CC   the antigen to raise the protection/immune response of a vaccinated
CC   individual. An example of the invention demonstrated the generation of a
CC   specific immune response against a melanoma-derived peptide (see
CC   ABP58360) by injection of mice with the peptide in combination with ODN
CC   16-A
XX
SQ   Sequence 10 BP; 0 A; 0 C; 0 G; 1 T; 1 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 8;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 135
ADJ56890
ID   ADJ56890 standard; DNA; 10 BP.
XX
AC   ADJ56890;
XX
DT   06-MAY-2004  (first entry)
```

XX
DE Antioxidant response element (ARE) consensus oligonucleotide.
XX
KW Rop; RopGAP; Cdc42/Rac-interactive binding motif; CRIB; plant phenotype;
KW ss; RHO-like small G-protein of plant; GAP; GTPase activating protein;
KW Rop GTPase; antioxidant response element ; ARE.
XX
OS Unidentified.
XX
PN US2004006783-A1.
XX
PD 08-JAN-2004.
XX
PF 13-JUN-2002; 2002US-00172526.
XX
PR 13-JUN-2002; 2002US-00172526.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Yang Z, Bailey-Serres J, Baxter-Burrell A, Wu G, Vernoud V;
XX
DR WPI; 2004-081756/08.
XX
PT New nucleic acid comprising a heterologous plant promoter operably linked
PT to a polynucleotide encoding a dominant negative RopGAP polypeptide,
PT useful for regulating Rop GTPase activity in plants.
XX
PS Disclosure; SEQ ID NO 15; 46pp; English.
XX
CC The invention relates to methods and compositions for regulating Rop (RHO
CC -like small G-protein of plant) GTPase activity in plant. The invention
CC also relates to RopGAP (GTPase activating protein) polypeptide which
CC inactivates Rop GTPase signaling and comprises of a Cdc42/Rac-interactive
CC binding (CRIB) motif and a GAP domain. The methods and compositions of
CC the invention are useful for regulating Rop GTPase activity in a plant.
CC The invention is useful for inducing expression of a particular RopGAP
CC nucleic acid to enhance or increase endogenous gene expression. Enhanced
CC expression can therefore be used to control plant phenotypes by
CC controlling Rop GTPase activity under RopGAP's control in desired
CC tissues, cells or subcellular locations. The present sequence is an
CC antioxidant response element (ARE) consensus oligonucleotide. This
CC sequence is used to illustrate the method of the invention.
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 1 T; 0 U; 2 Other;

```
  Query Match             30.0%;  Score 3;  DB 12;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          7 WWG 9
```

RESULT 136
ADJ56890/c
ID ADJ56890 standard; DNA; 10 BP.
XX
AC ADJ56890;
XX
DT 06-MAY-2004 (first entry)
XX
DE Antioxidant response element (ARE) consensus oligonucleotide.
XX
KW Rop; RopGAP; Cdc42/Rac-interactive binding motif; CRIB; plant phenotype;
KW ss; RHO-like small G-protein of plant; GAP; GTPase activating protein;
KW Rop GTPase; antioxidant response element ; ARE.
XX
OS Unidentified.
XX
PN US2004006783-A1.
XX
PD 08-JAN-2004.
XX
PF 13-JUN-2002; 2002US-00172526.
XX
PR 13-JUN-2002; 2002US-00172526.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Yang Z, Bailey-Serres J, Baxter-Burrell A, Wu G, Vernoud V;
XX
DR WPI; 2004-081756/08.
XX
PT New nucleic acid comprising a heterologous plant promoter operably linked
PT to a polynucleotide encoding a dominant negative RopGAP polypeptide,
PT useful for regulating Rop GTPase activity in plants.
XX
PS Disclosure; SEQ ID NO 15; 46pp; English.
XX
CC The invention relates to methods and compositions for regulating Rop (RHO
CC -like small G-protein of plant) GTPase activity in plant. The invention
CC also relates to RopGAP (GTPase activating protein) polypeptide which
CC inactivates Rop GTPase signaling and comprises of a Cdc42/Rac-interactive
CC binding (CRIB) motif and a GAP domain. The methods and compositions of
CC the invention are useful for regulating Rop GTPase activity in a plant.
CC The invention is useful for inducing expression of a particular RopGAP
CC nucleic acid to enhance or increase endogenous gene expression. Enhanced
CC expression can therefore be used to control plant phenotypes by
CC controlling Rop GTPase activity under RopGAP's control in desired
CC tissues, cells or subcellular locations. The present sequence is an
CC antioxidant response element (ARE) consensus oligonucleotide. This
CC sequence is used to illustrate the method of the invention.
XX
SQ Sequence 10 BP; 2 A; 2 C; 3 G; 1 T; 0 U; 2 Other;

```
  Query Match             30.0%;  Score 3;  DB 12;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          9 CWW 7
```

RESULT 137
ADN98340
ID ADN98340 standard; DNA; 10 BP.
XX
AC ADN98340;
XX
DT 29-JUL-2004 (first entry)
XX
DE Serum response factor binding sequence.
XX
KW ss; cytostatic; vulnerary; muscular;
KW megakaryocytic acute leukemia modulator; MAL modulator; MAL stimulator;
KW MAL inhibitor; MAL binding agent; serum response factor modulator;
KW SRF modulator; SRF stimulator; SRF inhibitor; SRF binding agent;
KW actin binding agent; antisense; RNAi; megakaryocytic acute leukemia;
KW cancer; leukemia; wounds; myopathy; muscle hypertrophy; angiogenesis;
KW metastasis.
XX
OS Unidentified.
XX
PN WO2004039980-A1.
XX
PD 13-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-GB004674.
XX
PR 30-OCT-2002; 2002US-0422420P.
XX
PA (CANC-) CANCER RES TECHNOLOGY LTD.
XX
PI Treisman RH, Miralles-Arenas F, Zaromytidou A, Posern G;

XX
DR WPI; 2004-400165/37.
XX
PT New agent that modulates megakaryocytic acute leukemia (MAL) activity,
PT useful for combating e.g., cancer, particularly acute myeloid leukemia
PT (AML-M7), wounds, or myopathies such as muscle hypertrophy.
XX
PS Disclosure; SEQ ID NO 1; 143pp; English.
XX
CC The invention relates to an agent that modulates a megakaryocytic acute
CC leukemia (MAL) activity. The agent or the polynucleotide that encodes the
CC agent is useful for combating a disorder in an individual by modulating
CC (either inhibiting or stimulating) a MAL activity, where the disorder is
CC cancer such as leukemia, particularly childhood leukemia AML-M7, wounds,
CC myopathies such as muscle hypertrophy, and any disorder that would
CC benefit from enhanced angiogenesis. In cancer, the agent combats tumor
CC cell growth, adhesion, cellular mobility, invasion or metastasis. The
CC agent may be administered as a polynucleotide The agent or the
CC polynucleotide that encodes the agent is useful in medicine and in the
CC manufacture of a medicament for combating the disorders above. The
CC agents, its encoding polynucleotide or the genetic construct is useful
CC for modulating an activity of MAL in vitro. This sequence corresponds to
CC the SRF binding site used in the method of the invention.
XX
SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
|||
Db 2 CWW 4

RESULT 138
ADN98340/c
ID ADN98340 standard; DNA; 10 BP.
XX
AC ADN98340;
XX
DT 29-JUL-2004 (first entry)
XX
DE Serum response factor binding sequence.
XX
KW ss; cytostatic; vulnerary; muscular;
KW megakaryocytic acute leukemia modulator; MAL modulator; MAL stimulator;
KW MAL inhibitor; MAL binding agent; serum response factor modulator;
KW SRF modulator; SRF stimulator; SRF inhibitor; SRF binding agent;
KW actin binding agent; antisense; RNAi; megakaryocytic acute leukemia;
KW cancer; leukemia; wounds; myopathy; muscle hypertrophy; angiogenesis;
KW metastasis.
XX
OS Unidentified.
XX
PN WO2004039980-A1.
XX
PD 13-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-GB004674.
XX
PR 30-OCT-2002; 2002US-0422420P.
XX
PA (CANC-) CANCER RES TECHNOLOGY LTD.
XX
PI Treisman RH, Miralles-Arenas F, Zaromytidou A, Posern G;
XX
DR WPI; 2004-400165/37.
XX
PT New agent that modulates megakaryocytic acute leukemia (MAL) activity,
PT useful for combating e.g., cancer, particularly acute myeloid leukemia
PT (AML-M7), wounds, or myopathies such as muscle hypertrophy.
XX
PS Disclosure; SEQ ID NO 1; 143pp; English.
XX
CC The invention relates to an agent that modulates a megakaryocytic acute
CC leukemia (MAL) activity. The agent or the polynucleotide that encodes the
CC agent is useful for combating a disorder in an individual by modulating
CC (either inhibiting or stimulating) a MAL activity, where the disorder is
CC cancer such as leukemia, particularly childhood leukemia AML-M7, wounds,
CC myopathies such as muscle hypertrophy, and any disorder that would
CC benefit from enhanced angiogenesis. In cancer, the agent combats tumor
CC cell growth, adhesion, cellular mobility, invasion or metastasis. The
CC agent may be administered as a polynucleotide The agent or the
CC polynucleotide that encodes the agent is useful in medicine and in the
CC manufacture of a medicament for combating the disorders above. The
CC agents, its encoding polynucleotide or the genetic construct is useful
CC for modulating an activity of MAL in vitro. This sequence corresponds to
CC the SRF binding site used in the method of the invention.
XX
SQ Sequence 10 BP; 0 A; 2 C; 2 G; 0 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
|||
Db 9 CWW 7

RESULT 139
AAT96077
ID AAT96077 standard; DNA; 11 BP.
XX
AC AAT96077;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 7; Col 17-18; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen

```
CC   cosmetics, foods and drugs. By using antisense sequences effective
CC   inhibition of both copies of a gene is possible, ensuring the substantial
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 11 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 7 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          8 RRR 10


RESULT 140
AAT96077/c
ID   AAT96077 standard; DNA; 11 BP.
XX
AC   AAT96077;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
PI   Jurka JW;
XX
DR   WPI; 1998-041303/04.
XX
PT   Genomic integration of DNA by site directed recombination - using
PT   construct containing recombination region homologous to consensus defined
PT   flanking region of short interspersed repeated DNA element.
XX
PS   Claim 7; Col 17-18; 12pp; English.
XX
CC   Integrating a DNA sequence into the genome of a vertebrate host cell,
CC   comprises introducing a construct comprising the DNA sequence and a
CC   recombination region homologous to a consensus defined flanking region of
CC   a short interspersed repeated DNA element (SINE), e.g. the present
CC   sequence. The method may be used to modify the phenotype of cells, or
CC   investigate the response of receptors, metabolic pathways or expression
CC   products involved in the regulation of transcription or transduction of
CC   signals. It may also be used to produce protein products and transgenic
CC   animals, by providing novel capabilities to the cells or inhibiting
CC   endogenous capabilities, investigate physiological indications and screen
CC   cosmetics, foods and drugs. By using antisense sequences effective
CC   inhibition of both copies of a gene is possible, ensuring the substantial
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 11 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 7 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         10 YYY 8


RESULT 141
ABA94933
ID   ABA94933 standard; DNA; 11 BP.
XX
AC   ABA94933;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human ecNOS gene nuclear factor Y (NFY_Q6) binding site DNA fragment.
XX
KW   Single nucleotide polymorphism; SNP; ecNOS; cytostatic; anti-diabetic;
KW   endothelial consecutive nitric oxide synthase; nephrotropic; hypotensive;
KW   cardiant; anti-atherosclerotic; vasoconstrictor; ophthalmalogical; human;
KW   tranquillizer; anxiolytic; anti-asthmatic; sedative; antiinflammatory;
KW   anticoagulant; osteopathic; cancer; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       8
FT                   /*tag=  a
FT                   /note= "SNP replaces the G in the core binding site with
FT                   an A at this position"
XX
PN   WO200208467-A1.
XX
PD   31-JAN-2002.
XX
PF   25-JUL-2001; 2001WO-US023321.
XX
PR   25-JUL-2000; 2000US-0220662P.
XX
PA   (DZGE-) DZ GENES LLC.
XX
PI   Moskowitz DW;
XX
DR   WPI; 2002-188635/24.
XX
PT   Diagnosing a genetic susceptibility for a disease, condition, or disorder
PT   in a subject comprises detecting the presence of a single nucleotide
PT   polymorphism in the endothelial consecutive nitric oxide synthase gene.
XX
PS   Example 5; Page 74; 97pp; English.
XX
CC   The invention relates to diagnosing a genetic susceptibility for a
CC   disease, condition, or disorder in a subject that comprises analysing a
CC   nucleic acid in a biological sample to detect the presence of a single
CC   nucleotide polymorphism (SNP) in the endothelial consecutive nitric oxide
CC   synthase (ecNOS) gene. The SNP is associated with a disease, condition or
CC   disorder selected from breast cancer, lung cancer, prostate cancer, non-
CC   insulin dependent diabetes, end stage renal disease due to non-insulin
CC   dependent diabetes or hypertension, hypertension, myocardial infarction,
CC   colon cancer, atherosclerotic peripheral vascular disease, cataracts,
CC   cerebrovascular accident, cardiomyopathy with hypertension, ischaemic
CC   cardiomyopathy, atrial fibrillation without valvular disease, alcohol
CC   abuse, anxiety, asthma, cholecystectomy, chronic obstructive pulmonary
CC   disease, degenerative joint disease and frequent de-clots and seizure
CC   disorder. The method is useful for diagnosing a genetic predisposition to
CC   a disease associated with SNPs, for designing a treatment regimen for a
CC   patient having a disease, condition or disorder caused either directly or
CC   indirectly by the presence of one or more SNPs. The present sequence
CC   represents the human ecNOS gene fragment where a polymorphism can occur
XX
SQ   Sequence 11 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
```

```
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYY 9
              |||
Db          8 GYY 10


RESULT 142
ABA94933/c
ID   ABA94933 standard; DNA; 11 BP.
XX
AC   ABA94933;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human ecNOS gene nuclear factor Y (NFY_Q6) binding site DNA fragment.
XX
KW   Single nucleotide polymorphism; SNP; ecNOS; cytostatic; anti-diabetic;
KW   endothelial consecutive nitric oxide synthase; nephrotropic; hypotensive;
KW   cardiant; anti-atherosclerotic; vasoconstrictor; ophthalmalogical; human;
KW   tranquillizer; anxiolytic; anti-asthmatic; sedative; antiinflammatory;
KW   anticoagulant; osteopathic; cancer; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       8
FT                   /*tag=  a
FT                   /note= "SNP replaces the G in the core binding site with
FT                   an A at this position"
XX
PN   WO200208467-A1.
XX
PD   31-JAN-2002.
XX
PF   25-JUL-2001; 2001WO-US023321.
XX
PR   25-JUL-2000; 2000US-0220662P.
XX
PA   (DZGE-) DZ GENES LLC.
XX
PI   Moskowitz DW;
XX
DR   WPI; 2002-188635/24.
XX
PT   Diagnosing a genetic susceptibility for a disease, condition, or disorder
PT   in a subject comprises detecting the presence of a single nucleotide
PT   polymorphism in the endothelial consecutive nitric oxide synthase gene.
XX
PS   Example 5; Page 74; 97pp; English.
XX
CC   The invention relates to diagnosing a genetic susceptibility for a
CC   disease, condition, or disorder in a subject that comprises analysing a
CC   nucleic acid in a biological sample to detect the presence of a single
CC   nucleotide polymorphism (SNP) in the endothelial consecutive nitric oxide
CC   synthase (ecNOS) gene. The SNP is associated with a disease, condition or
CC   disorder selected from breast cancer, lung cancer, prostate cancer, non-
CC   insulin dependent diabetes, end stage renal disease due to non-insulin
CC   dependent diabetes or hypertension, hypertension, myocardial infarction,
CC   colon cancer, atherosclerotic peripheral vascular disease, cataracts,
CC   cerebrovascular accident, cardiomyopathy with hypertension, ischaemic
CC   cardiomyopathy, atrial fibrillation without valvular disease, alcohol
CC   abuse, anxiety, asthma, cholecystectomy, chronic obstructive pulmonary
CC   disease, degenerative joint disease and frequent de-clots and seizure
CC   disorder. The method is useful for diagnosing a genetic predisposition to
CC   a disease associated with SNPs, for designing a treatment regimen for a
CC   patient having a disease, condition or disorder caused either directly or
CC   indirectly by the presence of one or more SNPs. The present sequence
CC   represents the human ecNOS gene fragment where a polymorphism can occur
XX
SQ   Sequence 11 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 5 Other;

  Query Match           30.0%;  Score 3;  DB 6;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db         10 RRC 8


RESULT 143
ADJ71749
ID   ADJ71749 standard; DNA; 11 BP.
XX
AC   ADJ71749;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Aptamer peptide display library inserted sequence end.
XX
KW   cytostatic; analgesic; anticonvulsant; cerebroprotective;
KW   antiparkinsonian; nootropic; neuroprotective; anti-HIV;
KW   modulator of cell phenotype; gene therapy; peptide aptamer;
KW   cell phenotype modification; peptide display library; cancer; pain;
KW   epilepsy; stroke; Parkinson's disease; Alzheimer's disease;
KW   Huntington's disease; multiple sclerosis; AIDS; ds; gene; ss.
XX
OS   Synthetic.
XX
PN   WO2003040168-A2.
XX
PD   15-MAY-2003.
XX
PF   06-NOV-2002; 2002WO-US035584.
XX
PR   06-NOV-2001; 2001US-0333262P.
PR   14-FEB-2002; 2002US-0357278P.
XX
PA   (ENAN-) ENANTA PHARM INC.
XX
PI   Benson JD,  Vincent SM,  Brasher BB,  Miao Z,  Lamming D;
XX
DR   WPI; 2003-541418/51.
XX
PT   Identifying peptide aptamer capable of modifying cell phenotype, by
PT   contacting cell sample with library encoding random peptide aptamers,
PT   selecting cell with altered phenotype, and identifying aptamers expressed
PT   in cell.
XX
PS   Example 1; SEQ ID NO 5; 173pp; English.
XX
CC   The invention relates to a method of identifying (M1) a peptide aptamer
CC   (PA) capable of modifying a cell phenotype, involving contacting a 1st
CC   sample of cells with a library of expressible nucleic acid sequences
CC   encoding random peptide aptamers linked to a fusion moiety, selecting at
CC   least one cell having an altered phenotype compared to the phenotype of
CC   the cell prior to contacting, and identifying peptide aptamers expressed
CC   in the selected cell. PA, its derivative or corresponding nucleic acid is
CC   useful for the molecular modelling of an agent having similar binding
CC   characteristics as PA. PA, its derivative or corresponding expressible
CC   nucleic acid is useful for treating or inhibiting a disease or condition
CC   (such as cancer) associated with an aberrant cell phenotype in a subject,
CC   where the aberrant cell phenotype is associated with a change in levels
CC   of apoptosis, viral resistance, signal transduction, protein trafficking,
CC   cell adhesion, membrane transport, cell motility, metabolic state or
CC   differentiation, when compared to a control cell, or the aberrant cell
CC   phenotype is associated with a tumor cell. The expressible nucleic acid
CC   is administered using a retrovirus that comprises a chromatin insulator
CC   element. PA is useful as a prognostic or diagnostic tool, for altering a
CC   cell phenotype, in gene therapy, as therapeutics for treating diseases
CC   (such as pain, epilepsy, stroke, Parkinson's disease, Alzheimer's
CC   disease, Huntington's disease, multiple sclerosis, AIDS), and for the
CC   research and development of other therapeutics. This sequence represents
CC   the end of the inserted sequence used to express the peptide display
CC   library (in retroviruses) and used to generate the aptamers of the
```

CC invention.
XX
SQ Sequence 11 BP; 2 A; 1 C; 2 G; 4 T; 0 U; 2 Other;

Query Match 30.0%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYY 9
||||
Db 2 GYY 4

RESULT 144
ADJ71749/c
ID ADJ71749 standard; DNA; 11 BP.
XX
AC ADJ71749;
XX
DT 06-MAY-2004 (first entry)
XX
DE Aptamer peptide display library inserted sequence end.
XX
KW cytostatic; analgesic; anticonvulsant; cerebroprotective;
KW antiparkinsonian; nootropic; neuroprotective; anti-HIV;
KW modulator of cell phenotype; gene therapy; peptide aptamer;
KW cell phenotype modification; peptide display library; cancer; pain;
KW epilepsy; stroke; Parkinson's disease; Alzheimer's disease;
KW Huntington's disease; multiple sclerosis; AIDS; ds; gene; ss.
XX
OS Synthetic.
XX
PN WO2003040168-A2.
XX
PD 15-MAY-2003.
XX
PF 06-NOV-2002; 2002WO-US035584.
XX
PR 06-NOV-2001; 2001US-0333262P.
PR 14-FEB-2002; 2002US-0357278P.
XX
PA (ENAN-) ENANTA PHARM INC.
XX
PI Benson JD, Vincent SM, Brasher BB, Miao Z, Lamming D;
XX
DR WPI; 2003-541418/51.
XX
PT Identifying peptide aptamer capable of modifying cell phenotype, by
PT contacting cell sample with library encoding random peptide aptamers,
PT selecting cell with altered phenotype, and identifying aptamers expressed
PT in cell.
XX
PS Example 1; SEQ ID NO 5; 173pp; English.
XX
CC The invention relates to a method of identifying (M1) a peptide aptamer
CC (PA) capable of modifying a cell phenotype, involving contacting a 1st
CC sample of cells with a library of expressible nucleic acid sequences
CC encoding random peptide aptamers linked to a fusion moiety, selecting at
CC least one cell having an altered phenotype compared to the phenotype of
CC the cell prior to contacting, and identifying peptide aptamers expressed
CC in the selected cell. PA, its derivative or corresponding nucleic acid is
CC useful for the molecular modelling of an agent having similar binding
CC characteristics as PA. PA, its derivative or corresponding expressible
CC nucleic acid is useful for treating or inhibiting a disease or condition
CC (such as cancer) associated with an aberrant cell phenotype in a subject,
CC where the aberrant cell phenotype is associated with a change in levels
CC of apoptosis, viral resistance, signal transduction, protein trafficking,
CC cell adhesion, membrane transport, cell motility, metabolic state or
CC differentiation, when compared to a control cell, or the aberrant cell
CC phenotype is associated with a tumor cell. The expressible nucleic acid
CC is administered using a retrovirus that comprises a chromatin insulator
CC element. PA is useful as a prognostic or diagnostic tool, for altering a
CC cell phenotype, in gene therapy, as therapeutics for treating diseases
CC (such as pain, epilepsy, stroke, Parkinson's disease, Alzheimer's
CC disease, Huntington's disease, multiple sclerosis, AIDS), and for the
CC research and development of other therapeutics. This sequence represents
CC the end of the inserted sequence used to express the peptide display
CC library (in retroviruses) and used to generate the aptamers of the
CC invention.
XX
SQ Sequence 11 BP; 2 A; 1 C; 2 G; 4 T; 0 U; 2 Other;

Query Match 30.0%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 4 RRC 2

RESULT 145
AAT04535
ID AAT04535 standard; DNA; 12 BP.
XX
AC AAT04535;
XX
DT 25-MAR-2003 (revised)
DT 07-DEC-1995 (first entry)
XX
DE Oxygen dependent repressor element.
XX
KW Oxygen dependent repressor; ODR; cytotoxic; hypoxic cell; ROX-1;
KW Tumour Necrosis Factor; TNF; SV-40; mammalian tumour cell; ss.
XX
OS Saccharomyces cerevisiae.
XX
PN WO9510273-A1.
XX
PD 20-APR-1995.
XX
PF 14-OCT-1994; 94WO-US011653.
XX
PR 14-OCT-1993; 93US-00137238.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Giaccia AJ, Koong AC;
XX
DR WPI; 1995-161549/21.
XX
PT Use of cpds. that activate protein kinase C activity - in hypoxic tumour
PT cells to mfr. a medicament for killing tumour cells.
XX
PS Disclosure; Fig 6a; 44pp; English.
XX
CC This sequence represents an oxygen dependent repressor (ODR) element.
CC This sequence is specifically bound by the repressor ROX-1. The sequence
CC is suitable for inclusion in a vector construct that is useful in the
CC invention. In this vector the ODR element is under the control of an SV-
CC 40 promoter. This vector induces (under the right conditions) synthesis
CC of a cytotoxic peptide product. The cytotoxic peptide product is Tumour
CC Necrosis Factor (TNF). The advantage of this vector is that it provides a
CC more versatile approach to selective killing of regions of hypoxic cells
CC in solid tumour than hyperthermic treatment of cells. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 12 BP; 1 A; 2 C; 1 G; 5 T; 0 U; 3 Other;

Query Match 30.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 146
AAT04535/c
ID AAT04535 standard; DNA; 12 BP.
XX
AC AAT04535;
XX
DT 25-MAR-2003 (revised)
DT 07-DEC-1995 (first entry)
XX
DE Oxygen dependent repressor element.
XX
KW Oxygen dependent repressor; ODR; cytotoxic; hypoxic cell; ROX-1;
KW Tumour Necrosis Factor; TNF; SV-40; mammalian tumour cell; ss.
XX
OS Saccharomyces cerevisiae.
XX
PN WO9510273-A1.
XX
PD 20-APR-1995.
XX
PF 14-OCT-1994; 94WO-US011653.
XX
PR 14-OCT-1993; 93US-00137238.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Giaccia AJ, Koong AC;
XX
DR WPI; 1995-161549/21.
XX
PT Use of cpds. that activate protein kinase C activity - in hypoxic tumour
PT cells to mfr. a medicament for killing tumour cells.
XX
PS Disclosure; Fig 6a; 44pp; English.
XX
CC This sequence represents an oxygen dependent repressor (ODR) element.
CC This sequence is specifically bound by the repressor ROX-1. The sequence
CC is suitable for inclusion in a vector construct that is useful in the
CC invention. In this vector the ODR element is under the control of an SV-
CC 40 promoter. This vector induces (under the right conditions) synthesis
CC of a cytotoxic peptide product. The cytotoxic peptide product is Tumour
CC Necrosis Factor (TNF). The advantage of this vector is that it provides a
CC more versatile approach to selective killing of regions of hypoxic cells
CC in solid tumour than hyperthermic treatment of cells. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 12 BP; 1 A; 2 C; 1 G; 5 T; 0 U; 3 Other;

Query Match 30.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 3 RRR 1

RESULT 147
AAT96066
ID AAT96066 standard; DNA; 12 BP.
XX
AC AAT96066;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 11-12; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 12 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 9 YYY 11

RESULT 148
AAT96066/c
ID AAT96066 standard; DNA; 12 BP.
XX
AC AAT96066;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX

PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 11-12; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 12 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 11 RRR 9

RESULT 149
AAT96078
ID AAT96078 standard; DNA; 12 BP.
XX
AC AAT96078;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 7; Col 17-18; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 12 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 9 RRR 11

RESULT 150
AAT96078/c
ID AAT96078 standard; DNA; 12 BP.
XX
AC AAT96078;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 7; Col 17-18; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial

```
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 12 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         11 YYY 9


RESULT 151
ADG88255
ID   ADG88255 standard; DNA; 12 BP.
XX
AC   ADG88255;
XX
DT   22-APR-2004  (first entry)
XX
DE   Pathogen infection-related gene consensus motif 1 cis element #697.
XX
KW   Pathogen infection-related gene; plant; Peronospora parasitica;
KW   defence mechanism; pathogen resistance; transgenic plant; oomycete;
KW   fungus; bacterium; virus; nematode; insect; aphid; promoter; cis element;
KW   motif 1; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200222675-A2.
XX
PD   21-MAR-2002.
XX
PF   14-SEP-2001; 2001WO-US028506.
XX
PR   15-SEP-2000; 2000US-0232778P.
PR   22-JUN-2001; 2001US-0300183P.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA   (UYNC-) UNIV NORTH CAROLINA.
PA   (GLAZ/) GLAZEBROOK J.
PA   (WANG/) WANG X.
PA   (DANG/) DANGL J L.
PA   (EULG/) EULGEM T.
PA   (ZHUT/) ZHU T.
XX
PI   Glazebrook J,  Wang X,  Dangl JL,  Eulgem T,  Zhu T;
XX
DR   WPI; 2002-292409/33.
XX
PT   Novel isolated polynucleotide, useful for conveying pathogen resistance
PT   to plants, and for identifying plants infected with a pathogen.
XX
PS   Claim 44; SEQ ID NO 697; 605pp; English.
XX
CC   The invention relates to 691 Arabidopsis thaliana genes (ADG87559--
CC   ADG87557}) whose expression is altered in response to pathogen infection,
CC   and to homologues of these genes from other plants or fungi, especially
CC   from maize, soybean, barley, alfalfa, sunflower, canola (oilseed rape),
CC   cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The
CC   expression of genes of the invention was upregulated or downregulated in
CC   Arabidopsis plants infected with the oomycete Peronospora parasitica,
CC   indicating that they play a role in defence mechanisms. The genes of the
CC   invention are regulated by RPP7 or RRP8 which act via unconventional
CC   signalling cascades, or by the RPP4-dependent pathway. The invention also
CC   relates to polypeptides encoded by the pathogen infection-related genes;
CC   promoter motifs from pathogen infection-related genes (ADG88243-ADG88327)
CC   ; expression cassettes, host cells and pathogen-resistant transgenic
CC   plants and their progeny comprising a polynucleotide of the invention;
CC   and a method of identifying a plant cell infected with a pathogen. The
CC   polynucleotide sequences and methods of the invention are useful for
CC   identifying plants infected with a pathogen, and for conferring
CC   resistance to pathogens such as oomycetes, fungi, bacteria, viruses,
CC   neamotodes and insects (e.g., aphids). The present sequence represents a
CC   consensus sequence for cis elements from the promoters of Arabidopsis
CC   thaliana genes whose expression is altered in response to Peronospora
CC   parasitica infection. Note: The sequence data for this patent can also be
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 12 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 2 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          6 CWW 8


RESULT 152
ADG88255/c
ID   ADG88255 standard; DNA; 12 BP.
XX
AC   ADG88255;
XX
DT   22-APR-2004  (first entry)
XX
DE   Pathogen infection-related gene consensus motif 1 cis element #697.
XX
KW   Pathogen infection-related gene; plant; Peronospora parasitica;
KW   defence mechanism; pathogen resistance; transgenic plant; oomycete;
KW   fungus; bacterium; virus; nematode; insect; aphid; promoter; cis element;
KW   motif 1; ds.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200222675-A2.
XX
PD   21-MAR-2002.
XX
PF   14-SEP-2001; 2001WO-US028506.
XX
PR   15-SEP-2000; 2000US-0232778P.
PR   22-JUN-2001; 2001US-0300183P.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA   (UYNC-) UNIV NORTH CAROLINA.
PA   (GLAZ/) GLAZEBROOK J.
PA   (WANG/) WANG X.
PA   (DANG/) DANGL J L.
PA   (EULG/) EULGEM T.
PA   (ZHUT/) ZHU T.
XX
PI   Glazebrook J,  Wang X,  Dangl JL,  Eulgem T,  Zhu T;
XX
DR   WPI; 2002-292409/33.
XX
PT   Novel isolated polynucleotide, useful for conveying pathogen resistance
PT   to plants, and for identifying plants infected with a pathogen.
XX
PS   Claim 44; SEQ ID NO 697; 605pp; English.
XX
CC   The invention relates to 691 Arabidopsis thaliana genes (ADG87559--
CC   ADG87557}) whose expression is altered in response to pathogen infection,
CC   and to homologues of these genes from other plants or fungi, especially
CC   from maize, soybean, barley, alfalfa, sunflower, canola (oilseed rape),
CC   cotton, peanut, sorghum, tobacco, sugarbeet, rice or wheat. The
CC   expression of genes of the invention was upregulated or downregulated in
CC   Arabidopsis plants infected with the oomycete Peronospora parasitica,
CC   indicating that they play a role in defence mechanisms. The genes of the
CC   invention are regulated by RPP7 or RRP8 which act via unconventional
```

CC signalling cascades, or by the RPP4-dependent pathway. The invention also
CC relates to polypeptides encoded by the pathogen infection-related genes;
CC promoter motifs from pathogen infection-related genes (ADG88243-ADG88327)
CC ; expression cassettes, host cells and pathogen-resistant transgenic
CC plants and their progeny comprising a polynucleotide of the invention;
CC and a method of identifying a plant cell infected with a pathogen. The
CC polynucleotide sequences and methods of the invention are useful for
CC identifying plants infected with a pathogen, and for conferring
CC resistance to pathogens such as oomycetes, fungi, bacteria, viruses,
CC neamotodes and insects (e.g., aphids). The present sequence represents a
CC consensus sequence for cis elements from the promoters of Arabidopsis
CC thaliana genes whose expression is altered in response to Peronospora
CC parasitica infection. Note: The sequence data for this patent can also be
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 12 BP; 3 A; 3 C; 1 G; 3 T; 0 U; 2 Other;

Query Match 30.0%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7
|||
Db 8 WWG 6

RESULT 153
ADB81333
ID ADB81333 standard; DNA; 12 BP.
XX
AC ADB81333;
XX
DT 04-DEC-2003 (first entry)
XX
DE Bacteriophage phi-C31 consensus splice acceptor site (SeqID 3).
XX
KW splice acceptor site; ss; phiC31 integrase; C31-Int;
KW site specific recombinase; SSR; gene function; disease model;
KW gene therapy; transgenic.
XX
OS Bacteriophage phi-C31.
XX
PN WO2003066867-A2.
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001122.
XX
PR 06-FEB-2002; 2002US-0354741P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Andreas S, Faust N;
XX
DR WPI; 2003-663599/62.
XX
PT New genetically engineered nucleic acid molecule, useful for preparing an
PT agent for recombining a DNA molecule containing phiC31 integrase
PT recognition sequences in a eukaryotic cell, a vertebrate or transgenic
PT organism.
XX
PS Claim 10; Page 40; 87pp; English.
XX
CC This invention relates to novel genetically engineered nucleic acid
CC molecules encoding phiC31 integrase (C31-Int), which has been codon
CC optimised for expression in eukaryotic host cells. The phiC31 integrase
CC is a site specific recombinase (SSR) that catalyzes recombination between
CC two phiC31 recognition sequences. The introduction of silent mutations
CC into the coding sequence changes the given codon to one that is most
CC frequently used in the respective host, which in turn alters expression
CC levels. Accordingly, using this ability to generate controlled and
CC permanent modifications in eukaryotic genomes has various research
CC applications including the study of gene function and the creation of
CC disease models, as well as gene therapy for medical applications, and the
CC design of economically important animals and crops. Furthermore, the
CC phiC31 integrase of the invention is useful for preparing an agent for
CC recombining a DNA molecule containing phiC31 integrase recognition
CC sequences in a eukaryotic cell, a vertebrate or transgenic organism. This
CC oligonucleotide sequence is bacteriophage phiC31 integrase consensus
CC splice accpetor site (SeqID 3) of the invention.
XX
SQ Sequence 12 BP; 1 A; 1 C; 2 G; 0 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 154
ADB81333/c
ID ADB81333 standard; DNA; 12 BP.
XX
AC ADB81333;
XX
DT 04-DEC-2003 (first entry)
XX
DE Bacteriophage phi-C31 consensus splice acceptor site (SeqID 3).
XX
KW splice acceptor site; ss; phiC31 integrase; C31-Int;
KW site specific recombinase; SSR; gene function; disease model;
KW gene therapy; transgenic.
XX
OS Bacteriophage phi-C31.
XX
PN WO2003066867-A2.
XX
PD 14-AUG-2003.
XX
PF 05-FEB-2003; 2003WO-EP001122.
XX
PR 06-FEB-2002; 2002US-0354741P.
XX
PA (ARTE-) ARTEMIS PHARM GMBH.
XX
PI Andreas S, Faust N;
XX
DR WPI; 2003-663599/62.
XX
PT New genetically engineered nucleic acid molecule, useful for preparing an
PT agent for recombining a DNA molecule containing phiC31 integrase
PT recognition sequences in a eukaryotic cell, a vertebrate or transgenic
PT organism.
XX
PS Claim 10; Page 40; 87pp; English.
XX
CC This invention relates to novel genetically engineered nucleic acid
CC molecules encoding phiC31 integrase (C31-Int), which has been codon
CC optimised for expression in eukaryotic host cells. The phiC31 integrase
CC is a site specific recombinase (SSR) that catalyzes recombination between
CC two phiC31 recognition sequences. The introduction of silent mutations
CC into the coding sequence changes the given codon to one that is most
CC frequently used in the respective host, which in turn alters expression
CC levels. Accordingly, using this ability to generate controlled and
CC permanent modifications in eukaryotic genomes has various research
CC applications including the study of gene function and the creation of
CC disease models, as well as gene therapy for medical applications, and the
CC design of economically important animals and crops. Furthermore, the
CC phiC31 integrase of the invention is useful for preparing an agent for
CC recombining a DNA molecule containing phiC31 integrase recognition
CC sequences in a eukaryotic cell, a vertebrate or transgenic organism. This
CC oligonucleotide sequence is bacteriophage phiC31 integrase consensus

```
CC   splice accpetor site (SeqID 3) of the invention.
XX
SQ   Sequence 12 BP; 1 A; 1 C; 2 G; 0 T; 0 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 10;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          7 RRR 5


RESULT 155
ADB81334
ID   ADB81334 standard; DNA; 12 BP.
XX
AC   ADB81334;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Bacteriophage phi-C31 consensus splice acceptor site (SeqID 4).
XX
KW   splice acceptor site; ss; phiC31 integrase; C31-Int;
KW   site specific recombinase; SSR; gene function; disease model;
KW   gene therapy; transgenic.
XX
OS   Bacteriophage phi-C31.
XX
PN   WO2003066867-A2.
XX
PD   14-AUG-2003.
XX
PF   05-FEB-2003; 2003WO-EP001122.
XX
PR   06-FEB-2002; 2002US-0354741P.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
XX
PI   Andreas S,  Faust N;
XX
DR   WPI; 2003-663599/62.
XX
PT   New genetically engineered nucleic acid molecule, useful for preparing an
PT   agent for recombining a DNA molecule containing phiC31 integrase
PT   recognition sequences in a eukaryotic cell, a vertebrate or transgenic
PT   organism.
XX
PS   Claim 10; Page 40; 87pp; English.
XX
CC   This invention relates to novel genetically engineered nucleic acid
CC   molecules encoding phiC31 integrase (C31-Int), which has been codon
CC   optimised for expression in eukaryotic host cells. The phiC31 integrase
CC   is a site specific recombinase (SSR) that catalyzes recombination between
CC   two phiC31 recognition sequences. The introduction of silent mutations
CC   into the coding sequence changes the given codon to one that is most
CC   frequently used in the respective host, which in turn alters expression
CC   levels. Accordingly, using this ability to generate controlled and
CC   permanent modifications in eukaryotic genomes has various research
CC   applications including the study of gene function and the creation of
CC   disease models, as well as gene therapy for medical applications, and the
CC   design of economically important animals and crops. Furthermore, the
CC   phiC31 integrase of the invention is useful for preparing an agent for
CC   recombining a DNA molecule containing phiC31 integrase recognition
CC   sequences in a eukaryotic cell, a vertebrate or transgenic organism. This
CC   oligonucleotide sequence is bacteriophage phiC31 integrase consensus
CC   splice accpetor site (SeqID 4) of the invention.
XX
SQ   Sequence 12 BP; 1 A; 0 C; 2 G; 1 T; 0 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 10;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          1 YYY 3


RESULT 156
ADB81334/c
ID   ADB81334 standard; DNA; 12 BP.
XX
AC   ADB81334;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Bacteriophage phi-C31 consensus splice acceptor site (SeqID 4).
XX
KW   splice acceptor site; ss; phiC31 integrase; C31-Int;
KW   site specific recombinase; SSR; gene function; disease model;
KW   gene therapy; transgenic.
XX
OS   Bacteriophage phi-C31.
XX
PN   WO2003066867-A2.
XX
PD   14-AUG-2003.
XX
PF   05-FEB-2003; 2003WO-EP001122.
XX
PR   06-FEB-2002; 2002US-0354741P.
XX
PA   (ARTE-) ARTEMIS PHARM GMBH.
XX
PI   Andreas S,  Faust N;
XX
DR   WPI; 2003-663599/62.
XX
PT   New genetically engineered nucleic acid molecule, useful for preparing an
PT   agent for recombining a DNA molecule containing phiC31 integrase
PT   recognition sequences in a eukaryotic cell, a vertebrate or transgenic
PT   organism.
XX
PS   Claim 10; Page 40; 87pp; English.
XX
CC   This invention relates to novel genetically engineered nucleic acid
CC   molecules encoding phiC31 integrase (C31-Int), which has been codon
CC   optimised for expression in eukaryotic host cells. The phiC31 integrase
CC   is a site specific recombinase (SSR) that catalyzes recombination between
CC   two phiC31 recognition sequences. The introduction of silent mutations
CC   into the coding sequence changes the given codon to one that is most
CC   frequently used in the respective host, which in turn alters expression
CC   levels. Accordingly, using this ability to generate controlled and
CC   permanent modifications in eukaryotic genomes has various research
CC   applications including the study of gene function and the creation of
CC   disease models, as well as gene therapy for medical applications, and the
CC   design of economically important animals and crops. Furthermore, the
CC   phiC31 integrase of the invention is useful for preparing an agent for
CC   recombining a DNA molecule containing phiC31 integrase recognition
CC   sequences in a eukaryotic cell, a vertebrate or transgenic organism. This
CC   oligonucleotide sequence is bacteriophage phiC31 integrase consensus
CC   splice accpetor site (SeqID 4) of the invention.
XX
SQ   Sequence 12 BP; 1 A; 0 C; 2 G; 1 T; 0 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 10;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          7 RRR 5


RESULT 157
```

```
AAT96067
ID   AAT96067 standard; DNA; 13 BP.
XX
AC   AAT96067;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
PI   Jurka JW;
XX
DR   WPI; 1998-041303/04.
XX
PT   Genomic integration of DNA by site directed recombination - using
PT   construct containing recombination region homologous to consensus defined
PT   flanking region of short interspersed repeated DNA element.
XX
PS   Claim 1; Col 13-14; 12pp; English.
XX
CC   Integrating a DNA sequence into the genome of a vertebrate host cell,
CC   comprises introducing a construct comprising the DNA sequence and a
CC   recombination region homologous to a consensus defined flanking region of
CC   a short interspersed repeated DNA element (SINE), e.g. the present
CC   sequence. The method may be used to modify the phenotype of cells, or
CC   investigate the response of receptors, metabolic pathways or expression
CC   products involved in the regulation of transcription or transduction of
CC   signals. It may also be used to produce protein products and transgenic
CC   animals, by providing novel capabilities to the cells or inhibiting
CC   endogenous capabilities, investigate physiological indications and screen
CC   cosmetics, foods and drugs. By using antisense sequences effective
CC   inhibition of both copies of a gene is possible, ensuring the substantial
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 13 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 7 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         10 YYY 12


RESULT 158
AAT96067/c
ID   AAT96067 standard; DNA; 13 BP.
XX
AC   AAT96067;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
PI   Jurka JW;
XX
DR   WPI; 1998-041303/04.
XX
PT   Genomic integration of DNA by site directed recombination - using
PT   construct containing recombination region homologous to consensus defined
PT   flanking region of short interspersed repeated DNA element.
XX
PS   Claim 1; Col 13-14; 12pp; English.
XX
CC   Integrating a DNA sequence into the genome of a vertebrate host cell,
CC   comprises introducing a construct comprising the DNA sequence and a
CC   recombination region homologous to a consensus defined flanking region of
CC   a short interspersed repeated DNA element (SINE), e.g. the present
CC   sequence. The method may be used to modify the phenotype of cells, or
CC   investigate the response of receptors, metabolic pathways or expression
CC   products involved in the regulation of transcription or transduction of
CC   signals. It may also be used to produce protein products and transgenic
CC   animals, by providing novel capabilities to the cells or inhibiting
CC   endogenous capabilities, investigate physiological indications and screen
CC   cosmetics, foods and drugs. By using antisense sequences effective
CC   inhibition of both copies of a gene is possible, ensuring the substantial
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 13 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 7 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         12 RRR 10


RESULT 159
AAT96079
ID   AAT96079 standard; DNA; 13 BP.
XX
AC   AAT96079;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
```

PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 7; Col 17-18; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 13 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 9 Other;

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 10 RRR 12

RESULT 160
AAT96079/c
ID AAT96079 standard; DNA; 13 BP.
XX
AC AAT96079;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 7; Col 17-18; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 13 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 9 Other;

Query Match 30.0%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 12 YYY 10

RESULT 161
ABL42250
ID ABL42250 standard; DNA; 13 BP.
XX
AC ABL42250;
XX
DT 29-AUG-2003 (revised)
DT 01-JUL-2002 (first entry)
XX
DE Animal cis-regulatory sequence from MBF-1.
XX
KW DNA fingerprinting; cancer; agriculture; breeding; PCR; primer;
KW gene family; ds.
XX
OS Metazoa.
XX
PN WO200162967-A2.
XX
PD 30-AUG-2001.
XX
PF 19-FEB-2001; 2001WO-IL000151.
XX
PR 22-FEB-2000; 2000IL-00134660.
PR 02-JUL-2000; 2000IL-00137124.
PR 20-AUG-2000; 2000IL-00137959.
XX
PA (GENE-) GENENA LTD.
PA (AGRI-) AGRIC RES ORG NEWE YA'AR RES CENTE.
XX
PI Vider B, Katzir N;
XX
DR WPI; 2002-239525/29.
XX
PT Polymerase chain reaction based method of DNA fingerprinting, useful for
PT analyzing genes, e.g. for identifying genes involved in cancer formation,
PT involves using a mix of primers that match the conserved regions of a
PT gene family.
XX
PS Example; Page 16; 28pp; English.
XX
CC The invention relates to a polymerase chain reaction (PCR) based method
CC of DNA fingerprinting, comprising using primers that match the conserved
CC regions of a gene family. The method is useful for gene expression
CC analysis of any cell or tissue, or for the performance of DNA
CC fingerprinting analysis of the same organism in order that one will

CC reveal the function of a gene that produced differential product between
CC genotypes. The method is also useful for identifying PCR reactions that
CC contain a gene of interest in a gene family reverse transcriptase (RT)-
CC PCR expression analysis. The method is also useful for identifying genes
CC that belong to a gene family that might be involved in cancer formation.
CC The method is particularly useful for comparing genomic sequences. These
CC are also applicable in agriculture (e.g. to mark useful genes to assist
CC breeding). The current sequence represents an animal cis-regulatory
CC sequence. This is used in DNA fingerprinting using primers or a mix of
CC primers that match the sequence of ubiquitous cis-acting regulatory
CC elements. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 13 BP; 7 A; 0 C; 0 G; 2 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 11 YYY 13

RESULT 162
ABL42250/c
ID ABL42250 standard; DNA; 13 BP.
XX
AC ABL42250;
XX
DT 29-AUG-2003 (revised)
DT 01-JUL-2002 (first entry)
XX
DE Animal cis-regulatory sequence from MBF-1.
XX
KW DNA fingerprinting; cancer; agriculture; breeding; PCR; primer;
KW gene family; ds.
XX
OS Metazoa.
XX
PN WO200162967-A2.
XX
PD 30-AUG-2001.
XX
PF 19-FEB-2001; 2001WO-IL000151.
XX
PR 22-FEB-2000; 2000IL-00134660.
PR 02-JUL-2000; 2000IL-00137124.
PR 20-AUG-2000; 2000IL-00137959.
XX
PA (GENE-) GENENA LTD.
PA (AGRI-) AGRIC RES ORG NEWE YA'AR RES CENTE.
XX
PI Vider B, Katzir N;
XX
DR WPI; 2002-239525/29.
XX
PT Polymerase chain reaction based method of DNA fingerprinting, useful for
PT analyzing genes, e.g. for identifying genes involved in cancer formation,
PT involves using a mix of primers that match the conserved regions of a
PT gene family.
XX
PS Example; Page 16; 28pp; English.
XX
CC The invention relates to a polymerase chain reaction (PCR) based method
CC of DNA fingerprinting, comprising using primers that match the conserved
CC regions of a gene family. The method is useful for gene expression
CC analysis of any cell or tissue, or for the performance of DNA
CC fingerprinting analysis of the same organism in order that one will
CC reveal the function of a gene that produced differential product between
CC genotypes. The method is also useful for identifying PCR reactions that
CC contain a gene of interest in a gene family reverse transcriptase (RT)-
CC PCR expression analysis. The method is also useful for identifying genes
CC that belong to a gene family that might be involved in cancer formation.
CC The method is particularly useful for comparing genomic sequences. These
CC are also applicable in agriculture (e.g. to mark useful genes to assist
CC breeding). The current sequence represents an animal cis-regulatory
CC sequence. This is used in DNA fingerprinting using primers or a mix of
CC primers that match the sequence of ubiquitous cis-acting regulatory
CC elements. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 13 BP; 7 A; 0 C; 0 G; 2 T; 0 U; 4 Other;

Query Match 30.0%; Score 3; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 13 RRR 11

RESULT 163
ADL71828
ID ADL71828 standard; DNA; 13 BP.
XX
AC ADL71828;
XX
DT 20-MAY-2004 (first entry)
XX
DE Anticancer agent-related Y-box DNA sequence.
XX
KW anticancer agent; cancer; decoy oligonucleotide; transcriptional factor;
KW YB-1 gene; ds; Y-box.
XX
OS Unidentified.
XX
PN KR2002025421-A.
XX
PD 04-APR-2002.
XX
PF 29-SEP-2000; 2000KR-00057192.
XX
PR 29-SEP-2000; 2000KR-00057192.
XX
PA (AHNB/) AHN B W.
PA (HANS/) HAN S W.
PA (KIMK/) KIM K K.
PA (KIMS/) KIM S J.
PA (SHIN/) SHIN B A.
XX
PI Ahn BW, Han SW, Jung SS, Kim KK, Kim SJ, Kim YR, Shin BA;
XX
DR WPI; 2003-500926/47.
XX
PT Composition of anticancer agent containing decoy oligonucleotides binding
PT to transcriptional factors of yb-1 gene.
XX
PS Disclosure; Page 3; 9pp; Korean.
XX
CC The invention comprises an anticancer agent containing decoy
CC oligonucleotides which bind to transcriptional factors of the YB-1 gene.
CC The decoy oligonucleotides selectively suppress the growth of cancer
CC cells without affecting normal cells. The present DNA sequence was used
CC in the exemplification of the invention.
XX
SQ Sequence 13 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 2 Other;

Query Match 30.0%; Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYY 9
|||
Db 9 GYY 11

```
RESULT 164
ADL71828/c
ID   ADL71828 standard; DNA; 13 BP.
XX
AC   ADL71828;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Anticancer agent-related Y-box DNA sequence.
XX
KW   anticancer agent; cancer; decoy oligonucleotide; transcriptional factor;
KW   YB-1 gene; ds; Y-box.
XX
OS   Unidentified.
XX
PN   KR2002025421-A.
XX
PD   04-APR-2002.
XX
PF   29-SEP-2000; 2000KR-00057192.
XX
PR   29-SEP-2000; 2000KR-00057192.
XX
PA   (AHNB/) AHN B W.
PA   (HANS/) HAN S W.
PA   (KIMK/) KIM K K.
PA   (KIMS/) KIM S J.
PA   (SHIN/) SHIN B A.
XX
PI   Ahn BW,  Han SW,  Jung SS,  Kim KK,  Kim SJ,  Kim YR,  Shin BA;
XX
DR   WPI; 2003-500926/47.
XX
PT   Composition of anticancer agent containing decoy oligonucleotides binding
PT   to transcriptional factors of yb-1 gene.
XX
PS   Disclosure; Page 3; 9pp; Korean.
XX
CC   The invention comprises an anticancer agent containing decoy
CC   oligonucleotides which bind to transcriptional factors of the YB-1 gene.
CC   The decoy oligonucleotides selectively suppress the growth of cancer
CC   cells without affecting normal cells. The present DNA sequence was used
CC   in the exemplification of the invention.
XX
SQ   Sequence 13 BP; 3 A; 2 C; 3 G; 3 T; 0 U; 2 Other;

  Query Match             30.0%;  Score 3;  DB 11;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db         11 RRC 9


RESULT 165
ACC85667
ID   ACC85667 standard; DNA; 13 BP.
XX
AC   ACC85667;
XX
DT   22-APR-2004  (first entry)
XX
DE   RNA ligand aptamer marker/probe NCW13.
XX
KW   RNA aptamer; ligand; heat shock factor protein; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2004001065-A2.
XX
PD   31-DEC-2003.
XX
PF   24-JUN-2003; 2003WO-US019966.
XX
PR   24-JUN-2002; 2002US-0391255P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Shi H,  Lis JT;
XX
DR   WPI; 2004-071741/07.
XX
PT   Identifying RNA ligands that bind to a target molecule comprises treating
PT   a first pool of RNA ligands that collectively bind more than one target
PT   to reduce the concentration or eliminate the presence of target-binding
PT   RNA ligands.
XX
PS   Example 1; Page 64; 0pp; English.
XX
CC   The present invention relates to a method of identifying RNA ligands that
CC   bind to a target molecule, comprising treating a first pool of RNA
CC   ligands that collectively bind more than one target under conditions
CC   effective to reduce the concentration or eliminate the presence of one or
CC   more predominate target-binding RNA ligands from the first pool of RNA
CC   ligands. In particular, the method can be used to identify RNA aptamers
CC   capable of binding to heat shock factor protein. The present sequence is
CC   a DNA sequence shown in the exemplification of the invention
XX
SQ   Sequence 13 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 7 Other;

  Query Match             30.0%;  Score 3;  DB 12;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          5 CWW 7


RESULT 166
ACC85667/c
ID   ACC85667 standard; DNA; 13 BP.
XX
AC   ACC85667;
XX
DT   22-APR-2004  (first entry)
XX
DE   RNA ligand aptamer marker/probe NCW13.
XX
KW   RNA aptamer; ligand; heat shock factor protein; PCR; primer; ss.
XX
OS   Synthetic.
XX
PN   WO2004001065-A2.
XX
PD   31-DEC-2003.
XX
PF   24-JUN-2003; 2003WO-US019966.
XX
PR   24-JUN-2002; 2002US-0391255P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Shi H,  Lis JT;
XX
DR   WPI; 2004-071741/07.
XX
PT   Identifying RNA ligands that bind to a target molecule comprises treating
PT   a first pool of RNA ligands that collectively bind more than one target
PT   to reduce the concentration or eliminate the presence of target-binding
PT   RNA ligands.
XX
PS   Example 1; Page 64; 0pp; English.
XX
CC   The present invention relates to a method of identifying RNA ligands that
```

```
CC   bind to a target molecule, comprising treating a first pool of RNA
CC   ligands that collectively bind more than one target under conditions
CC   effective to reduce the concentration or eliminate the presence of one or
CC   more predominate target-binding RNA ligands from the first pool of RNA
CC   ligands. In particular, the method can be used to identify RNA aptamers
CC   capable of binding to heat shock factor protein. The present sequence is
CC   a DNA sequence shown in the exemplification of the invention
XX
SQ   Sequence 13 BP; 0 A; 6 C; 0 G; 0 T; 0 U; 7 Other;

  Query Match             30.0%;  Score 3;  DB 12;  Length 13;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          7 WWG 5


RESULT 167
AAQ80951
ID   AAQ80951 standard; RNA; 14 BP.
XX
AC   AAQ80951;
XX
DT   27-FEB-1996  (first entry)
XX
DE   HIV protease inhibitory oligoribonucleotide sequence (d).
XX
KW   Human immunodeficiency virus; HIV; protease; inhibitor; gene therapy;
KW   diagnostic probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .14
FT                   /*tag=  a
FT                   /note= "each nucleotide is opt. modified"
XX
PN   WO9429479-A1.
XX
PD   22-DEC-1994.
XX
PF   09-JUN-1994;   94WO-US006456.
XX
PR   09-JUN-1993;   93US-00073873.
XX
PA   (PHAR-) PHARMAGENICS INC.
XX
PI   Beutel BA,  Sherman MI,  Coppola GR;
XX
DR   WPI; 1995-036501/05.
XX
PT   Inhibiting HIV protease function with specific oligonucleotides - which
PT   bind to the enzyme, for treating or preventing HIV infection, including
PT   use of vectors in gene therapy.
XX
PS   Claim 4; Page 51; 81pp; English.
XX
CC   HIV protease function is inhibited by RNA oligonucleotides which include
CC   one of the sequences 5'-AANGU, 5'-ANUGGA, 5'-AGUGUG, 5'-UNGAUNY, 5'-CCUC,
CC   5'-GGUGNA or one of the sequences in AAQ80950- AAQ80953. Oligonucleotides
CC   contg. these sequences are found to bind to HIV protease and so prevent
CC   HIV maturation. Prefd. oligoribonucleotides are classified into classes A
CC   (AAQ80954-Q80964), B (AAQ80965-Q80967) and C (AAQ80968-Q80972) and can be
CC   single- or double- stranded or in the form of a stem-loop structure, a
CC   pseudoknot or a closed, circular structure. In addition to their
CC   potential use in gene therapy, the oligonucleotides will be useful as
CC   diagnostic probes to detect HIV infection
XX
SQ   Sequence 14 BP; 4 A; 1 C; 5 G; 0 T; 1 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         12 RRR 14


RESULT 168
AAQ80951/c
ID   AAQ80951 standard; RNA; 14 BP.
XX
AC   AAQ80951;
XX
DT   27-FEB-1996  (first entry)
XX
DE   HIV protease inhibitory oligoribonucleotide sequence (d).
XX
KW   Human immunodeficiency virus; HIV; protease; inhibitor; gene therapy;
KW   diagnostic probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .14
FT                   /*tag=  a
FT                   /note= "each nucleotide is opt. modified"
XX
PN   WO9429479-A1.
XX
PD   22-DEC-1994.
XX
PF   09-JUN-1994;   94WO-US006456.
XX
PR   09-JUN-1993;   93US-00073873.
XX
PA   (PHAR-) PHARMAGENICS INC.
XX
PI   Beutel BA,  Sherman MI,  Coppola GR;
XX
DR   WPI; 1995-036501/05.
XX
PT   Inhibiting HIV protease function with specific oligonucleotides - which
PT   bind to the enzyme, for treating or preventing HIV infection, including
PT   use of vectors in gene therapy.
XX
PS   Claim 4; Page 51; 81pp; English.
XX
CC   HIV protease function is inhibited by RNA oligonucleotides which include
CC   one of the sequences 5'-AANGU, 5'-ANUGGA, 5'-AGUGUG, 5'-UNGAUNY, 5'-CCUC,
CC   5'-GGUGNA or one of the sequences in AAQ80950- AAQ80953. Oligonucleotides
CC   contg. these sequences are found to bind to HIV protease and so prevent
CC   HIV maturation. Prefd. oligoribonucleotides are classified into classes A
CC   (AAQ80954-Q80964), B (AAQ80965-Q80967) and C (AAQ80968-Q80972) and can be
CC   single- or double- stranded or in the form of a stem-loop structure, a
CC   pseudoknot or a closed, circular structure. In addition to their
CC   potential use in gene therapy, the oligonucleotides will be useful as
CC   diagnostic probes to detect HIV infection
XX
SQ   Sequence 14 BP; 4 A; 1 C; 5 G; 0 T; 1 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         14 YYY 12


RESULT 169
AAQ80974
ID   AAQ80974 standard; DNA; 14 BP.
```

```
XX
AC   AAQ80974;
XX
DT   27-FEB-1996  (first entry)
XX
DE   HIV protease inhibitory oligodeoxyribonucleotide sequence (n).
XX
KW   Human immunodeficiency virus; HIV; protease; inhibitor; gene therapy;
KW   diagnostic probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .14
FT                   /*tag=  a
FT                   /note= "each nucleotide is opt. modified"
XX
PN   WO9429479-A1.
XX
PD   22-DEC-1994.
XX
PF   09-JUN-1994;   94WO-US006456.
XX
PR   09-JUN-1993;   93US-00073873.
XX
PA   (PHAR-) PHARMAGENICS INC.
XX
PI   Beutel BA,  Sherman MI,  Coppola GR;
XX
DR   WPI; 1995-036501/05.
XX
PT   Inhibiting HIV protease function with specific oligonucleotides - which
PT   bind to the enzyme, for treating or preventing HIV infection, including
PT   use of vectors in gene therapy.
XX
PS   Claim 12; Page 54; 81pp; English.
XX
CC   HIV protease function is inhibited by DNA oligonucleotides which include
CC   one of the sequences 5'-AANGT, 5'-ANTGGA, 5'-AGTGTG, 5'-TNGATNY, 5'-CCTC,
CC   5'-GGTGNA or one of the sequences in AAQ80973- AAQ80976. Oligonucleotides
CC   contg. these sequences are found to bind to HIV protease and so prevent
CC   HIV maturation. Prefd. oligo- deoxyribonucleotides are classified into
CC   classes D (AAQ80977-Q80987), E (AAQ80988-Q80990) and F (AAQ80991-Q80995)
CC   and can be single- or double- stranded or in the form of a stem-loop
CC   structure, a pseudoknot or a closed, circular structure. In addition to
CC   their potential use in gene therapy, the oligonucleotides will be useful
CC   as diagnostic probes to detect HIV infection
XX
SQ   Sequence 14 BP; 4 A; 1 C; 5 G; 1 T; 0 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         12 RRR 14


RESULT 170
AAQ80974/c
ID   AAQ80974 standard; DNA; 14 BP.
XX
AC   AAQ80974;
XX
DT   27-FEB-1996  (first entry)
XX
DE   HIV protease inhibitory oligodeoxyribonucleotide sequence (n).
XX
KW   Human immunodeficiency virus; HIV; protease; inhibitor; gene therapy;
KW   diagnostic probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 1. .14
FT                   /*tag=  a
FT                   /note= "each nucleotide is opt. modified"
XX
PN   WO9429479-A1.
XX
PD   22-DEC-1994.
XX
PF   09-JUN-1994;   94WO-US006456.
XX
PR   09-JUN-1993;   93US-00073873.
XX
PA   (PHAR-) PHARMAGENICS INC.
XX
PI   Beutel BA,  Sherman MI,  Coppola GR;
XX
DR   WPI; 1995-036501/05.
XX
PT   Inhibiting HIV protease function with specific oligonucleotides - which
PT   bind to the enzyme, for treating or preventing HIV infection, including
PT   use of vectors in gene therapy.
XX
PS   Claim 12; Page 54; 81pp; English.
XX
CC   HIV protease function is inhibited by DNA oligonucleotides which include
CC   one of the sequences 5'-AANGT, 5'-ANTGGA, 5'-AGTGTG, 5'-TNGATNY, 5'-CCTC,
CC   5'-GGTGNA or one of the sequences in AAQ80973- AAQ80976. Oligonucleotides
CC   contg. these sequences are found to bind to HIV protease and so prevent
CC   HIV maturation. Prefd. oligo- deoxyribonucleotides are classified into
CC   classes D (AAQ80977-Q80987), E (AAQ80988-Q80990) and F (AAQ80991-Q80995)
CC   and can be single- or double- stranded or in the form of a stem-loop
CC   structure, a pseudoknot or a closed, circular structure. In addition to
CC   their potential use in gene therapy, the oligonucleotides will be useful
CC   as diagnostic probes to detect HIV infection
XX
SQ   Sequence 14 BP; 4 A; 1 C; 5 G; 1 T; 0 U; 3 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         14 YYY 12


RESULT 171
AAT96068
ID   AAT96068 standard; DNA; 14 BP.
XX
AC   AAT96068;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
```

PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 13-14; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 14 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 11 YYY 13

RESULT 172
AAT96068/c
ID AAT96068 standard; DNA; 14 BP.
XX
AC AAT96068;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 13-14; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 14 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 13 RRR 11

RESULT 173
AAT96080
ID AAT96080 standard; DNA; 14 BP.
XX
AC AAT96080;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 7; Col 17-18; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial

```
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 10 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         11 RRR 13


RESULT 174
AAT96080/c
ID   AAT96080 standard; DNA; 14 BP.
XX
AC   AAT96080;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
PI   Jurka JW;
XX
DR   WPI; 1998-041303/04.
XX
PT   Genomic integration of DNA by site directed recombination - using
PT   construct containing recombination region homologous to consensus defined
PT   flanking region of short interspersed repeated DNA element.
XX
PS   Claim 7; Col 17-18; 12pp; English.
XX
CC   Integrating a DNA sequence into the genome of a vertebrate host cell,
CC   comprises introducing a construct comprising the DNA sequence and a
CC   recombination region homologous to a consensus defined flanking region of
CC   a short interspersed repeated DNA element (SINE), e.g. the present
CC   sequence. The method may be used to modify the phenotype of cells, or
CC   investigate the response of receptors, metabolic pathways or expression
CC   products involved in the regulation of transcription or transduction of
CC   signals. It may also be used to produce protein products and transgenic
CC   animals, by providing novel capabilities to the cells or inhibiting
CC   endogenous capabilities, investigate physiological indications and screen
CC   cosmetics, foods and drugs. By using antisense sequences effective
CC   inhibition of both copies of a gene is possible, ensuring the substantial
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 14 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 10 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         13 YYY 11


RESULT 175
AAV22311
ID   AAV22311 standard; cDNA; 14 BP.
XX
AC   AAV22311;
XX
DT   29-JUN-1998  (first entry)
XX
DE   ISRE gene promoter motif found in a trophoblast STAT utron.
XX
KW   Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;
KW   interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW   antigen expression; gene promoter; class I; class II; IFN signalling;
KW   GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-1;
KW   B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment;
KW   autoimmune disease; inflammatory disease; ss.
XX
OS   Unidentified.
XX
PN   WO9744450-A1.
XX
PD   27-NOV-1997.
XX
PF   21-MAY-1997;   97WO-US009459.
XX
PR   21-MAY-1996;   96US-00646789.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Peyman JA;
XX
DR   WPI; 1998-018505/02.
XX
PT   Utrons, RNA molecules containing promoter regulatory motifs - useful to
PT   suppress express expression from promoter of interest, specifically TSU
PT   nucleic acid suppression of MHC Class I and II gene expression.
XX
PS   Disclosure; Page 89; 200pp; English.
XX
CC   The present sequence represents an ISRE gene promoter motif found in a
CC   trophoblast STAT utron (TSU). TSUs be isolated from a CDNA library
CC   prepared from mRNA isolated from trophoblast cells. Utrons are from, or
CC   are homologous to, the 3' untranslated region (UTR), of an mRNA that
CC   stimulates or inhibits a cellular response by sequence specific
CC   interactions. The TSU is able to suppress constitutive and interferon-
CC   gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I
CC   and class II antigen expression and expression of other antigens, the
CC   gene promoters of which contain related sequence motifs that are
CC   stimulated by the same factors which stimulate MHC class I and class II
CC   antigen expression. The TSU sequence contains motifs related to IFN
CC   signalling (GAS, ISRE and interleukin-4 response elements). The nucleic
CC   acid can be used to regulate gene expression in a subject, e.g. a human
CC   or a cell in vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7
CC   -1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be used to
CC   inhibit transplant rejection, or treat an autoimmune or inflammatory
CC   disease or disorder. It can also be used to inhibit the action of STAT1-
CC   6, or a cytokine
XX
SQ   Sequence 14 BP; 1 A; 1 C; 1 G; 5 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         11 YYY 13
```

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RESULT 176
AAV22311/c
ID   AAV22311 standard; cDNA; 14 BP.
XX
AC   AAV22311;
XX
DT   29-JUN-1998  (first entry)
XX
DE   ISRE gene promoter motif found in a trophoblast STAT utron.
XX
KW   Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;
KW   interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW   antigen expression; gene promoter; class I; class II; IFN signalling;
KW   GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-1;
KW   B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment;
KW   autoimmune disease; inflammatory disease; ss.
XX
OS   Unidentified.
XX
PN   WO9744450-A1.
XX
PD   27-NOV-1997.
XX
PF   21-MAY-1997;   97WO-US009459.
XX
PR   21-MAY-1996;   96US-00646789.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Peyman JA;
XX
DR   WPI; 1998-018505/02.
XX
PT   Utrons, RNA molecules containing promoter regulatory motifs - useful to
PT   suppress express expression from promoter of interest, specifically TSU
PT   nucleic acid suppression of MHC Class I and II gene expression.
XX
PS   Disclosure; Page 89; 200pp; English.
XX
CC   The present sequence represents an ISRE gene promoter motif found in a
CC   trophoblast STAT utron (TSU). TSUs be isolated from a CDNA library
CC   prepared from mRNA isolated from trophoblast cells. Utrons are from, or
CC   are homologous to, the 3' untranslated region (UTR), of an mRNA that
CC   stimulates or inhibits a cellular response by sequence specific
CC   interactions. The TSU is able to suppress constitutive and interferon-
CC   gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I
CC   and class II antigen expression and expression of other antigens, the
CC   gene promoters of which contain related sequence motifs that are
CC   stimulated by the same factors which stimulate MHC class I and class II
CC   antigen expression. The TSU sequence contains motifs related to IFN
CC   signalling (GAS, ISRE and interleukin-4 response elements). The nucleic
CC   acid can be used to regulate gene expression in a subject, e.g. a human
CC   or a cell in vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7
CC   -1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be used to
CC   inhibit transplant rejection, or treat an autoimmune or inflammatory
CC   disease or disorder. It can also be used to inhibit the action of STAT1-
CC   6, or a cytokine
XX
SQ   Sequence 14 BP; 1 A; 1 C; 1 G; 5 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         14 RRR 12


RESULT 177
AAV22312
ID   AAV22312 standard; RNA; 14 BP.
XX
AC   AAV22312;
XX
DT   29-JUN-1998  (first entry)
XX
DE   ISRE complement sequence found in the TSUs of the invention.
XX
KW   Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;
KW   interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW   antigen expression; gene promoter; class I; class II; IFN signalling;
KW   GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-1;
KW   B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment;
KW   autoimmune disease; inflammatory disease; ss.
XX
OS   Unidentified.
XX
PN   WO9744450-A1.
XX
PD   27-NOV-1997.
XX
PF   21-MAY-1997;   97WO-US009459.
XX
PR   21-MAY-1996;   96US-00646789.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Peyman JA;
XX
DR   WPI; 1998-018505/02.
XX
PT   Utrons, RNA molecules containing promoter regulatory motifs - useful to
PT   suppress express expression from promoter of interest, specifically TSU
PT   nucleic acid suppression of MHC Class I and II gene expression.
XX
PS   Disclosure; Page 89; 200pp; English.
XX
CC   The present sequence represents an ISRE complement sequence found in the
CC   trophoblast STAT utrons (TSUs) of the invention. Utrons are from, or are
CC   homologous to, the 3' untranslated region (UTR), of an mRNA that
CC   stimulates or inhibits a cellular response by sequence specific
CC   interactions. The TSU is able to suppress constitutive and interferon-
CC   gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I
CC   and class II antigen expression and expression of other antigens, the
CC   gene promoters of which contain related sequence motifs that are
CC   stimulated by the same factors which stimulate MHC class I and class II
CC   antigen expression. The TSU sequence contains motifs related to IFN
CC   signalling (GAS, ISRE and interleukin-4 response elements). The nucleic
CC   acid can be used to regulate gene expression in a subject, e.g. a human
CC   or a cell in vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7
CC   -1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be used to
CC   inhibit transplant rejection, or treat an autoimmune or inflammatory
CC   disease or disorder. It can also be used to inhibit the action of STAT1-
CC   6, or a cytokine
XX
SQ   Sequence 14 BP; 5 A; 1 C; 1 G; 1 T; 0 U; 6 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          1 RRR 3


RESULT 178
AAV22312/c
ID   AAV22312 standard; RNA; 14 BP.
XX
AC   AAV22312;
XX
DT   29-JUN-1998  (first entry)
XX
DE   ISRE complement sequence found in the TSUs of the invention.
```

XX
KW Trophoblast STAT utron; TSU; 3' untranslated region; UTR; inhibition;
KW interferon-gamma; IFN-gamma; major histocompatibility complex; MHC;
KW antigen expression; gene promoter; class I; class II; IFN signalling;
KW GAS; ISRE; interleukin-4 response element; gene expression; ICAM-7; B7-1;
KW B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment;
KW autoimmune disease; inflammatory disease; ss.
XX
OS Unidentified.
XX
PN WO9744450-A1.
XX
PD 27-NOV-1997.
XX
PF 21-MAY-1997; 97WO-US009459.
XX
PR 21-MAY-1996; 96US-00646789.
XX
PA (UYYA) UNIV YALE.
XX
PI Peyman JA;
XX
DR WPI; 1998-018505/02.
XX
PT Utrons, RNA molecules containing promoter regulatory motifs - useful to
PT suppress express expression from promoter of interest, specifically TSU
PT nucleic acid suppression of MHC Class I and II gene expression.
XX
PS Disclosure; Page 89; 200pp; English.
XX
CC The present sequence represents an ISRE complement sequence found in the
CC trophoblast STAT utrons (TSUs) of the invention. Utrons are from, or are
CC homologous to, the 3' untranslated region (UTR), of an mRNA that
CC stimulates or inhibits a cellular response by sequence specific
CC interactions. The TSU is able to suppress constitutive and interferon-
CC gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I
CC and class II antigen expression and expression of other antigens, the
CC gene promoters of which contain related sequence motifs that are
CC stimulated by the same factors which stimulate MHC class I and class II
CC antigen expression. The TSU sequence contains motifs related to IFN
CC signalling (GAS, ISRE and interleukin-4 response elements). The nucleic
CC acid can be used to regulate gene expression in a subject, e.g. a human
CC or a cell in vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7
CC -1, B7-2, Fc gamma R, IL-2 or HIV gene expression. It can be used to
CC inhibit transplant rejection, or treat an autoimmune or inflammatory
CC disease or disorder. It can also be used to inhibit the action of STAT1-
CC 6, or a cytokine
XX
SQ Sequence 14 BP; 5 A; 1 C; 1 G; 1 T; 0 U; 6 Other;

Query Match 30.0%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 4 YYY 2

RESULT 179
AAZ43723
ID AAZ43723 standard; DNA; 14 BP.
XX
AC AAZ43723;
XX
DT 24-FEB-2000 (first entry)
XX
DE Human FSH-beta splice-acceptor site DNA motif.
XX
KW FSH-beta; human; follicle stimulating hormone-beta; gene therapy;
KW delivery system; treatment; infertility; fertility enhancer; ss.
XX
OS Homo sapiens.
XX
PN WO9957263-A1.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-US009795.
XX
PR 07-MAY-1998; 98US-0084663P.
XX
PA (TRAN-) TRANSKARYOTIC THERAPIES INC.
XX
PI Treco DA, Heartlein MW, Selden RF;
XX
DR WPI; 2000-052968/04.
XX
PT Novel DNA construct used to produce recombinant cells useful for in vitro
PT protein production and gene therapy.
XX
PS Disclosure; Page 64; 70pp; English.
XX
CC This invention describes a novel DNA construct (A) that alters expression
CC of an endogenous follicle stimulating hormone (FSH)-beta gene in a
CC mammalian cell upon integration into the genome of the cell via
CC homologous recombination. Homologously recombinant cells of the invention
CC which express follicle-stimulating hormone beta (FSHbeta) are useful for
CC in vitro production of the protein and gene therapy. The cells are also
CC useful as populations of homologously recombinant cell lines, as
CC populations of homologously recombinant primary or secondary cells, as
CC homologously recombinant clonal cells or strains, as homologously
CC recombinant heterogeneous cell strains or lines, and as cell mixtures of
CC any of the above. Such cells may be used in a delivery system for
CC treating infertility, for enhancing fertility in a human or animal, or
CC for treating any other conditions treatable with FSHbeta. The
CC polynucleotides may be used as a source of primers, and to alter the
CC expression of an endogenous FSHbeta gene. This sequence represents a
CC human FSH-beta gene splice-acceptor site DNA motif which is used in the
CC method of the invention
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 0 T; 0 U; 12 Other;

Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 180
AAZ43723/c
ID AAZ43723 standard; DNA; 14 BP.
XX
AC AAZ43723;
XX
DT 24-FEB-2000 (first entry)
XX
DE Human FSH-beta splice-acceptor site DNA motif.
XX
KW FSH-beta; human; follicle stimulating hormone-beta; gene therapy;
KW delivery system; treatment; infertility; fertility enhancer; ss.
XX
OS Homo sapiens.
XX
PN WO9957263-A1.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-US009795.
XX
PR 07-MAY-1998; 98US-0084663P.
XX
PA (TRAN-) TRANSKARYOTIC THERAPIES INC.

```
XX
PI   Treco DA,  Heartlein MW,  Selden RF;
XX
DR   WPI; 2000-052968/04.
XX
PT   Novel DNA construct used to produce recombinant cells useful for in vitro
PT   protein production and gene therapy.
XX
PS   Disclosure; Page 64; 70pp; English.
XX
CC   This invention describes a novel DNA construct (A) that alters expression
CC   of an endogenous follicle stimulating hormone (FSH)-beta gene in a
CC   mammalian cell upon integration into the genome of the cell via
CC   homologous recombination. Homologously recombinant cells of the invention
CC   which express follicle-stimulating hormone beta (FSHbeta) are useful for
CC   in vitro production of the protein and gene therapy. The cells are also
CC   useful as populations of homologously recombinant cell lines, as
CC   populations of homologously recombinant primary or secondary cells, as
CC   homologously recombinant clonal cells or strains, as homologously
CC   recombinant heterogeneous cell strains or lines, and as cell mixtures of
CC   any of the above. Such cells may be used in a delivery system for
CC   treating infertility, for enhancing fertility in a human or animal, or
CC   for treating any other conditions treatable with FSHbeta. The
CC   polynucleotides may be used as a source of primers, and to alter the
CC   expression of an endogenous FSHbeta gene. This sequence represents a
CC   human FSH-beta gene splice-acceptor site DNA motif which is used in the
CC   method of the invention
XX
SQ   Sequence 14 BP; 1 A; 0 C; 1 G; 0 T; 0 U; 12 Other;

  Query Match             30.0%;  Score 3;  DB 3;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 181
AAA91879
ID   AAA91879 standard; DNA; 14 BP.
XX
AC   AAA91879;
XX
DT   08-JAN-2001  (first entry)
XX
DE   Complement of SNP site beginning at position 211 of the TGF-b1 gene.
XX
KW   TGF b1; promoter region; gene therapy; end-stage renal disease; ESRD;
KW   single nucleotide polymorphism; SNP; human; primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(6,G)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200049169-A1.
XX
PD   24-AUG-2000.
XX
PF   18-FEB-2000; 2000WO-US004251.
XX
PR   19-FEB-1999;   99US-0120787P.
XX
PA   (DZGE-) DZGENES LLC.
XX
PI   Moskowitz DW;
XX
DR   WPI; 2000-549279/50.
XX
PT   Diagnosing genetic susceptibility for end-stage renal disease using
PT   single nucleotide polymorphisms, involves analyzing sample obtained from
PT   subject to detect genetic polymorphism in the sample polynucleotide.
XX
PS   Example 3; Page 37; 73pp; English.
XX
CC   The present invention relates the diagnosis of genetic susceptibility for
CC   end-stage renal disease (ESRD). The method involves analysing a
CC   polynucleotide sample for a single nucleotide polymorphism (SNP)
CC   associated with an altered susceptibility for ESRD. The method allows
CC   early detection of ESRD and hence effective delay or ideally, prevention
CC   of ESRD is made possible. The present sequence is a SNP site found in the
CC   human TGF-b1 promoter sequence (see AAA91866). Polymorphisms in this gene
CC   are known to be a probable trigger for renal apoptosis
XX
SQ   Sequence 14 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 3;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          6 YYY 8


RESULT 182
AAA91879/c
ID   AAA91879 standard; DNA; 14 BP.
XX
AC   AAA91879;
XX
DT   08-JAN-2001  (first entry)
XX
DE   Complement of SNP site beginning at position 211 of the TGF-b1 gene.
XX
KW   TGF b1; promoter region; gene therapy; end-stage renal disease; ESRD;
KW   single nucleotide polymorphism; SNP; human; primer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(6,G)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200049169-A1.
XX
PD   24-AUG-2000.
XX
PF   18-FEB-2000; 2000WO-US004251.
XX
PR   19-FEB-1999;   99US-0120787P.
XX
PA   (DZGE-) DZGENES LLC.
XX
PI   Moskowitz DW;
XX
DR   WPI; 2000-549279/50.
XX
PT   Diagnosing genetic susceptibility for end-stage renal disease using
PT   single nucleotide polymorphisms, involves analyzing sample obtained from
PT   subject to detect genetic polymorphism in the sample polynucleotide.
XX
PS   Example 3; Page 37; 73pp; English.
XX
CC   The present invention relates the diagnosis of genetic susceptibility for
CC   end-stage renal disease (ESRD). The method involves analysing a
CC   polynucleotide sample for a single nucleotide polymorphism (SNP)
CC   associated with an altered susceptibility for ESRD. The method allows
CC   early detection of ESRD and hence effective delay or ideally, prevention
CC   of ESRD is made possible. The present sequence is a SNP site found in the
CC   human TGF-b1 promoter sequence (see AAA91866). Polymorphisms in this gene
```

CC are known to be a probable trigger for renal apoptosis
XX
SQ Sequence 14 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 8 RRR 6

RESULT 183
AAD17448
ID AAD17448 standard; DNA; 14 BP.
XX
AC AAD17448;
XX
DT 10-DEC-2001 (first entry)
XX
DE Splice acceptor site which directs the splicing of one exon to another.
XX
KW Mutation; homologous recombination; target sequence; gene therapy;
KW homologous recombination-enhancing agent; non-homologous end joining;
KW therapeutic protein; splice acceptor site; ds.
XX
OS Unidentified.
XX
PN WO200168882-A2.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US007870.
XX
PR 14-MAR-2000; 2000US-00525160.
XX
PA (TRAN-) TRANSKARYOTIC THERAPIES INC.
XX
PI Ivanov E;
XX
DR WPI; 2001-582459/65.
XX
PT Complex or composition comprising a double stranded DNA sequence, a
PT homologous recombination-enhancing agent, and agent inhibiting non-
PT homologous end joining, for promoting alteration of a target sequence in
PT a cell.
XX
PS Disclosure; Page 50; 82pp; English.
XX
CC The invention relates to a complex for promoting alteration of a target
CC sequence in a cell, comprising a double stranded DNA sequence, a
CC homologous recombination-enhancing agent and an agent inhibiting non-
CC homologous end joining. The invention is used in gene therapy. The
CC complex is useful for promoting an alteration at a selected site of a
CC target sequence of a cell preferably of fungal, plant or animal origin,
CC or of vertebrate origin which is a primary or secondary mammalian (human)
CC cell or an immortalised mammalian (human) cell, where target sequence
CC comprises a mutation preferably point mutation having less than 10 base
CC pairs which differ from wild-type sequence, (selected from cystic
CC fibrosis transmembrane regulator (CFTR) gene having mutation changes in
CC an amino acid encoded by codon 508, beta-globin gene having mutation
CC changes in an amino acid encoded by codon 6, Factor VIII gene having
CC mutation changes in an amino acid encoded by codon 2209 or 2229, Factor
CC IX gene, von Willebrand factor gene or xeroderma pigmentosa group G gene)
CC ; and the DNA sequence comprises a wild-type sequence which can correct
CC the mutation. The method further comprises introducing an agent which
CC inhibits a mismatch-repair protein (expression), which is from Msh2,
CC Msh6, Msh3, M1h1 and PMS2, or is an anti-mismatch-repair protein antibody
CC covalently linked to the DNA sequence, or to Rad52 protein or its
CC fragment. The complex is useful for altering expression of a protein
CC coding sequence of a gene in a cell. The method comprises introducing the
CC complex into the cell, where the DNA sequence comprises a regulatory
CC sequence, maintaining the cell under conditions which permit alteration
CC of a targetted genomic sequence to produce a homologously recombinant
CC cell and maintaining the homologously recombinant cell under conditions
CC which permit expression of the protein coding sequence of the gene under
CC control of the regulatory sequence. Homologously recombinant cell is
CC useful as a vehicle or delivery system for therapeutic proteins, such as
CC enzymes, hormones, cytokines, antigens, antibodies, clotting factors,
CC anti-sense RNA, regulatory proteins, transcription proteins, receptors,
CC structural proteins, novel (non-optimised) proteins and nucleic acid
CC products and engineered DNA and for supplying a therapeutic protein,
CC including erythropoietin, calcitonin, growth hormone, insulin and
CC insulinotropin. The present sequence is a splice acceptor site, used in
CC the invention. This sequence directs the splicing of one exon to another
CC exon
XX
SQ Sequence 14 BP; 1 A; 0 C; 1 G; 0 T; 0 U; 12 Other;

Query Match 30.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 184
AAD17448/c
ID AAD17448 standard; DNA; 14 BP.
XX
AC AAD17448;
XX
DT 10-DEC-2001 (first entry)
XX
DE Splice acceptor site which directs the splicing of one exon to another.
XX
KW Mutation; homologous recombination; target sequence; gene therapy;
KW homologous recombination-enhancing agent; non-homologous end joining;
KW therapeutic protein; splice acceptor site; ds.
XX
OS Unidentified.
XX
PN WO200168882-A2.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US007870.
XX
PR 14-MAR-2000; 2000US-00525160.
XX
PA (TRAN-) TRANSKARYOTIC THERAPIES INC.
XX
PI Ivanov E;
XX
DR WPI; 2001-582459/65.
XX
PT Complex or composition comprising a double stranded DNA sequence, a
PT homologous recombination-enhancing agent, and agent inhibiting non-
PT homologous end joining, for promoting alteration of a target sequence in
PT a cell.
XX
PS Disclosure; Page 50; 82pp; English.
XX
CC The invention relates to a complex for promoting alteration of a target
CC sequence in a cell, comprising a double stranded DNA sequence, a
CC homologous recombination-enhancing agent and an agent inhibiting non-
CC homologous end joining. The invention is used in gene therapy. The
CC complex is useful for promoting an alteration at a selected site of a
CC target sequence of a cell preferably of fungal, plant or animal origin,
CC or of vertebrate origin which is a primary or secondary mammalian (human)
CC cell or an immortalised mammalian (human) cell, where target sequence
CC comprises a mutation preferably point mutation having less than 10 base
CC pairs which differ from wild-type sequence, (selected from cystic

```
CC   fibrosis transmembrane regulator (CFTR) gene having mutation changes in
CC   an amino acid encoded by codon 508, beta-globin gene having mutation
CC   changes in an amino acid encoded by codon 6, Factor VIII gene having
CC   mutation changes in an amino acid encoded by codon 2209 or 2229, Factor
CC   IX gene, von Willebrand factor gene or xeroderma pigmentosa group G gene)
CC   ; and the DNA sequence comprises a wild-type sequence which can correct
CC   the mutation. The method further comprises introducing an agent which
CC   inhibits a mismatch-repair protein (expression), which is from Msh2,
CC   Msh6, Msh3, M1h1 and PMS2, or is an anti-mismatch-repair protein antibody
CC   covalently linked to the DNA sequence, or to Rad52 protein or its
CC   fragment. The complex is useful for altering expression of a protein
CC   coding sequence of a gene in a cell. The method comprises introducing the
CC   complex into the cell, where the DNA sequence comprises a regulatory
CC   sequence, maintaining the cell under conditions which permit alteration
CC   of a targetted genomic sequence to produce a homologously recombinant
CC   cell and maintaining the homologously recombinant cell under conditions
CC   which permit expression of the protein coding sequence of the gene under
CC   control of the regulatory sequence. Homologously recombinant cell is
CC   useful as a vehicle or delivery system for therapeutic proteins, such as
CC   enzymes, hormones, cytokines, antigens, antibodies, clotting factors,
CC   anti-sense RNA, regulatory proteins, transcription proteins, receptors,
CC   structural proteins, novel (non-optimised) proteins and nucleic acid
CC   products and engineered DNA and for supplying a therapeutic protein,
CC   including erythropoietin, calcitonin, growth hormone, insulin and
CC   insulinotropin. The present sequence is a splice acceptor site, used in
CC   the invention. This sequence directs the splicing of one exon to another
CC   exon
XX
SQ   Sequence 14 BP; 1 A; 0 C; 1 G; 0 T; 0 U; 12 Other;

  Query Match             30.0%;  Score 3;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 185
ABA99069
ID   ABA99069 standard; DNA; 14 BP.
XX
AC   ABA99069;
XX
DT   03-JUL-2002  (first entry)
XX
DE   Gut-enriched Krueppel-like factor binding site (complementary strand).
XX
KW   TGF-beta 1; transforming growth factor-beta 1; cytostatic; hypotensive;
KW   cardiant; vasotropic; antiarteriosclerotic; antidiabetic; nephrotropic;
KW   antialcoholic; tranquilliser; antiasthmatic; gene therapy; cancer;
KW   hypertension; GKLF; gut-enriched Krueppel-like factor; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(6,G)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "This is a SNP in the human TGFbeta1 promoter"
XX
PN   WO200208468-A1.
XX
PD   31-JAN-2002.
XX
PF   25-JUL-2001; 2001WO-US023368.
XX
PR   25-JUL-2000; 2000US-0220583P.
XX
PA   (DZGE-) DZ GENES LLC.
XX
PI   Moskowitz DW;
XX
DR   WPI; 2002-241578/29.
XX
PT   Novel nucleic acid molecule comprising a single nucleotide polymorphism
PT   at a specified position in transforming growth factor-beta 1 promoter
PT   region, useful for diagnosing cancers, hypertension and other diseases.
XX
PS   Example 2; Page 38; 67pp; English.
XX
CC   The sequence represents the complement of the human transforming growth
CC   factor-beta 1 promoter region gut-enriched Krueppel-like factor (GKLF)
CC   site. The invention relates to a novel isolated polynucleotide containing
CC   at least one single nucleotide polymorphism (SNP) at position 216 or 563
CC   of TGF-beta1, where the SNP is associated with a disease, condition or
CC   disorder. The polynucleotide has cytostatic, hypotensive, cardiant,
CC   vasotropic, antiarteriosclerotic, antidiabetic, nephrotropic,
CC   antialcoholic, tranquilliser, and antiasthmatic activity. The
CC   polynucleotide may have a use in gene therapy. The method provided in the
CC   invention is useful for diagnosing genetic susceptibility for cancers,
CC   hypertension and a variety of other diseases. The polynucleotide is
CC   useful for designing prophylactic treatment regimes for patients
CC   determined to have an increased susceptibility to these diseases
XX
SQ   Sequence 14 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 6;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          6 YYY 8


RESULT 186
ABA99069/c
ID   ABA99069 standard; DNA; 14 BP.
XX
AC   ABA99069;
XX
DT   03-JUL-2002  (first entry)
XX
DE   Gut-enriched Krueppel-like factor binding site (complementary strand).
XX
KW   TGF-beta 1; transforming growth factor-beta 1; cytostatic; hypotensive;
KW   cardiant; vasotropic; antiarteriosclerotic; antidiabetic; nephrotropic;
KW   antialcoholic; tranquilliser; antiasthmatic; gene therapy; cancer;
KW   hypertension; GKLF; gut-enriched Krueppel-like factor; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   variation       replace(6,G)
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
FT                   /note= "This is a SNP in the human TGFbeta1 promoter"
XX
PN   WO200208468-A1.
XX
PD   31-JAN-2002.
XX
PF   25-JUL-2001; 2001WO-US023368.
XX
PR   25-JUL-2000; 2000US-0220583P.
XX
PA   (DZGE-) DZ GENES LLC.
XX
PI   Moskowitz DW;
XX
DR   WPI; 2002-241578/29.
XX
PT   Novel nucleic acid molecule comprising a single nucleotide polymorphism
PT   at a specified position in transforming growth factor-beta 1 promoter
```

PT region, useful for diagnosing cancers, hypertension and other diseases.
XX
PS Example 2; Page 38; 67pp; English.
XX
CC The sequence represents the complement of the human transforming growth
CC factor-beta 1 promoter region gut-enriched Krueppel-like factor (GKLF)
CC site. The invention relates to a novel isolated polynucleotide containing
CC at least one single nucleotide polymorphism (SNP) at position 216 or 563
CC of TGF-beta1, where the SNP is associated with a disease, condition or
CC disorder. The polynucleotide has cytostatic, hypotensive, cardiant,
CC vasotropic, antiarteriosclerotic, antidiabetic, nephrotropic,
CC antialcoholic, tranquilliser, and antiasthmatic activity. The
CC polynucleotide may have a use in gene therapy. The method provided in the
CC invention is useful for diagnosing genetic susceptibility for cancers,
CC hypertension and a variety of other diseases. The polynucleotide is
CC useful for designing prophylactic treatment regimes for patients
CC determined to have an increased susceptibility to these diseases
XX
SQ Sequence 14 BP; 0 A; 2 C; 0 G; 4 T; 0 U; 8 Other;

Query Match 30.0%; Score 3; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 8 RRR 6

RESULT 187
ADF83663
ID ADF83663 standard; DNA; 14 BP.
XX
AC ADF83663;
XX
DT 26-FEB-2004 (first entry)
XX
DE Pravastatin production related primer, P450R2.
XX
KW mevastatin; pravastatin; lactone ring-closed body; ss; primer.
XX
OS Unidentified.
XX
PN JP2002247984-A.
XX
PD 03-SEP-2002.
XX
PF 23-FEB-2001; 2001JP-00047664.
XX
PR 23-FEB-2001; 2001JP-00047664.
XX
PA (SAOC) MERCIAN CORP.
XX
DR WPI; 2004-084761/09.
XX
PT A DNA participating in the production of pravastatin, a recombinant
PT plasmid, a transformant, production of pravastatin.
XX
PS Example 1; SEQ ID NO 4; 15pp; Japanese.
XX
CC The invention relates to novel isolated pure DNA containing a gene
CC participating in the biological conversion of mevastatin to pravastatin,
CC its salt or its lactone ring-closed body or a mutant having a function of
CC hybridizing with the gene under a stringent condition and giving the
CC conversion activity to Streptomyces lividans. The invention further
CC relates to an isolated pure DNA containing a gene participating in the
CC biological conversion of mevastatin, its lactone ring-open body or its
CC salt which can be prepared from a microbe of Microtetraspora genus to
CC pravastatin, its salt or its lactone ring-closed body or a mutant having
CC a function of hybridizing with the gene under a stringent condition and
CC giving the conversion activity to Streptomyces lividans. The method is
CC used for the preparation of pravastatin, its salt or its lactone ring-
CC closed body. This polynucleotide sequence represents a primer relating to
CC the production of pravastatin of the invention.
XX
SQ Sequence 14 BP; 2 A; 3 C; 1 G; 3 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 11 RRC 13

RESULT 188
ADF83663/c
ID ADF83663 standard; DNA; 14 BP.
XX
AC ADF83663;
XX
DT 26-FEB-2004 (first entry)
XX
DE Pravastatin production related primer, P450R2.
XX
KW mevastatin; pravastatin; lactone ring-closed body; ss; primer.
XX
OS Unidentified.
XX
PN JP2002247984-A.
XX
PD 03-SEP-2002.
XX
PF 23-FEB-2001; 2001JP-00047664.
XX
PR 23-FEB-2001; 2001JP-00047664.
XX
PA (SAOC) MERCIAN CORP.
XX
DR WPI; 2004-084761/09.
XX
PT A DNA participating in the production of pravastatin, a recombinant
PT plasmid, a transformant, production of pravastatin.
XX
PS Example 1; SEQ ID NO 4; 15pp; Japanese.
XX
CC The invention relates to novel isolated pure DNA containing a gene
CC participating in the biological conversion of mevastatin to pravastatin,
CC its salt or its lactone ring-closed body or a mutant having a function of
CC hybridizing with the gene under a stringent condition and giving the
CC conversion activity to Streptomyces lividans. The invention further
CC relates to an isolated pure DNA containing a gene participating in the
CC biological conversion of mevastatin, its lactone ring-open body or its
CC salt which can be prepared from a microbe of Microtetraspora genus to
CC pravastatin, its salt or its lactone ring-closed body or a mutant having
CC a function of hybridizing with the gene under a stringent condition and
CC giving the conversion activity to Streptomyces lividans. The method is
CC used for the preparation of pravastatin, its salt or its lactone ring-
CC closed body. This polynucleotide sequence represents a primer relating to
CC the production of pravastatin of the invention.
XX
SQ Sequence 14 BP; 2 A; 3 C; 1 G; 3 T; 0 U; 5 Other;

Query Match 30.0%; Score 3; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYY 9
|||
Db 13 GYY 11

RESULT 189
AAT96081
ID AAT96081 standard; DNA; 15 BP.

```
XX
AC   AAT96081;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
PI   Jurka JW;
XX
DR   WPI; 1998-041303/04.
XX
PT   Genomic integration of DNA by site directed recombination - using
PT   construct containing recombination region homologous to consensus defined
PT   flanking region of short interspersed repeated DNA element.
XX
PS   Claim 7; Col 17-18; 12pp; English.
XX
CC   Integrating a DNA sequence into the genome of a vertebrate host cell,
CC   comprises introducing a construct comprising the DNA sequence and a
CC   recombination region homologous to a consensus defined flanking region of
CC   a short interspersed repeated DNA element (SINE), e.g. the present
CC   sequence. The method may be used to modify the phenotype of cells, or
CC   investigate the response of receptors, metabolic pathways or expression
CC   products involved in the regulation of transcription or transduction of
CC   signals. It may also be used to produce protein products and transgenic
CC   animals, by providing novel capabilities to the cells or inhibiting
CC   endogenous capabilities, investigate physiological indications and screen
CC   cosmetics, foods and drugs. By using antisense sequences effective
CC   inhibition of both copies of a gene is possible, ensuring the substantial
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 11 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         12 RRR 14


RESULT 190
AAT96081/c
ID   AAT96081 standard; DNA; 15 BP.
XX
AC   AAT96081;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
PI   Jurka JW;
XX
DR   WPI; 1998-041303/04.
XX
PT   Genomic integration of DNA by site directed recombination - using
PT   construct containing recombination region homologous to consensus defined
PT   flanking region of short interspersed repeated DNA element.
XX
PS   Claim 7; Col 17-18; 12pp; English.
XX
CC   Integrating a DNA sequence into the genome of a vertebrate host cell,
CC   comprises introducing a construct comprising the DNA sequence and a
CC   recombination region homologous to a consensus defined flanking region of
CC   a short interspersed repeated DNA element (SINE), e.g. the present
CC   sequence. The method may be used to modify the phenotype of cells, or
CC   investigate the response of receptors, metabolic pathways or expression
CC   products involved in the regulation of transcription or transduction of
CC   signals. It may also be used to produce protein products and transgenic
CC   animals, by providing novel capabilities to the cells or inhibiting
CC   endogenous capabilities, investigate physiological indications and screen
CC   cosmetics, foods and drugs. By using antisense sequences effective
CC   inhibition of both copies of a gene is possible, ensuring the substantial
CC   absence of the particular transcriptional or translational product. In
CC   addition the method may enhance efficiency in gene therapy, when
CC   providing for a capability in which the host is deficient
XX
SQ   Sequence 15 BP; 0 A; 0 C; 0 G; 4 T; 0 U; 11 Other;

  Query Match             30.0%;  Score 3;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         14 YYY 12


RESULT 191
AAT96069
ID   AAT96069 standard; DNA; 15 BP.
XX
AC   AAT96069;
XX
DT   31-MAR-1998  (first entry)
XX
DE   Recombination region homologous to SINE flanking region.
XX
KW   Recombination region; consensus defined flanking region;
KW   short interspersed repeated DNA element; SINE; ss.
XX
OS   Synthetic.
XX
PN   US5695977-A.
XX
PD   09-DEC-1997.
XX
PF   07-MAY-1996;   96US-00643886.
XX
PR   31-AUG-1995;   95US-0003063P.
XX
PA   (GENE-) GENETIC INFORMATION RES INST.
XX
```

PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 13-14; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 15 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 9 Other;

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          8 YYY 10
              |||
Db         12 YYY 14
```

RESULT 192
AAT96069/c
ID AAT96069 standard; DNA; 15 BP.
XX
AC AAT96069;
XX
DT 31-MAR-1998 (first entry)
XX
DE Recombination region homologous to SINE flanking region.
XX
KW Recombination region; consensus defined flanking region;
KW short interspersed repeated DNA element; SINE; ss.
XX
OS Synthetic.
XX
PN US5695977-A.
XX
PD 09-DEC-1997.
XX
PF 07-MAY-1996; 96US-00643886.
XX
PR 31-AUG-1995; 95US-0003063P.
XX
PA (GENE-) GENETIC INFORMATION RES INST.
XX
PI Jurka JW;
XX
DR WPI; 1998-041303/04.
XX
PT Genomic integration of DNA by site directed recombination - using
PT construct containing recombination region homologous to consensus defined
PT flanking region of short interspersed repeated DNA element.
XX
PS Claim 1; Col 13-14; 12pp; English.
XX
CC Integrating a DNA sequence into the genome of a vertebrate host cell,
CC comprises introducing a construct comprising the DNA sequence and a
CC recombination region homologous to a consensus defined flanking region of
CC a short interspersed repeated DNA element (SINE), e.g. the present
CC sequence. The method may be used to modify the phenotype of cells, or
CC investigate the response of receptors, metabolic pathways or expression
CC products involved in the regulation of transcription or transduction of
CC signals. It may also be used to produce protein products and transgenic
CC animals, by providing novel capabilities to the cells or inhibiting
CC endogenous capabilities, investigate physiological indications and screen
CC cosmetics, foods and drugs. By using antisense sequences effective
CC inhibition of both copies of a gene is possible, ensuring the substantial
CC absence of the particular transcriptional or translational product. In
CC addition the method may enhance efficiency in gene therapy, when
CC providing for a capability in which the host is deficient
XX
SQ Sequence 15 BP; 4 A; 0 C; 0 G; 2 T; 0 U; 9 Other;

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RRR 3
              |||
Db         14 RRR 12
```

RESULT 193
AAF75852
ID AAF75852 standard; DNA; 15 BP.
XX
AC AAF75852;
XX
DT 18-MAY-2001 (first entry)
XX
DE 3' splice junction consensus sequence used to design PCR primers.
XX
KW 3' splice junction consensus sequence; PCR primer design; ds.
XX
OS Unidentified.
XX
PN WO200116350-A1.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-US024122.
XX
PR 01-SEP-1999; 99US-0151975P.
PR 01-NOV-1999; 99US-00431451.
XX
PA (GENO-) GENOME TECHNOLOGIES LLC.
XX
PI Senapathy P;
XX
DR WPI; 2001-226695/23.
XX
PT Amplifying desired regions of nucleic acid, especially exons from a
PT genomic DNA sample, comprises using a partly-fixed consensus first primer
PT and partly-fixed second primer, both having a sequence of randomized
PT nucleotides.
XX
PS Disclosure; Fig 2; 52pp; English.
XX
CC The present invention relates to a method for amplifying a region of
CC nucleic acid from a sample via PCR using several primers. The primers of
CC the present invention have a region of fixed nucleotide sequence
CC identical or complementary to a consensus sequence of interest and also
CC have a region of randomised nucleotide sequence. The present sequence is
CC the 3' splice junction consensus sequence, which was used to design PCR
CC primers for use in the present invention. The method is useful for
CC specifically amplifying a desired region of a nucleic acid, especially
CC exons from a sample of DNA. The method is also applicable for amplifying
CC regions flanking a consensus sequence in a sample of nucleic acid of
CC totally or partially unknown sequence

```
XX
SQ   Sequence 15 BP; 1 A; 0 C; 2 G; 3 T; 0 U; 9 Other;

  Query Match             30.0%;  Score 3;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          5 YYY 7


RESULT 194
AAF75852/c
ID   AAF75852 standard; DNA; 15 BP.
XX
AC   AAF75852;
XX
DT   18-MAY-2001  (first entry)
XX
DE   3' splice junction consensus sequence used to design PCR primers.
XX
KW   3' splice junction consensus sequence; PCR primer design; ds.
XX
OS   Unidentified.
XX
PN   WO200116350-A1.
XX
PD   08-MAR-2001.
XX
PF   01-SEP-2000; 2000WO-US024122.
XX
PR   01-SEP-1999;   99US-0151975P.
PR   01-NOV-1999;   99US-00431451.
XX
PA   (GENO-) GENOME TECHNOLOGIES LLC.
XX
PI   Senapathy P;
XX
DR   WPI; 2001-226695/23.
XX
PT   Amplifying desired regions of nucleic acid, especially exons from a
PT   genomic DNA sample, comprises using a partly-fixed consensus first primer
PT   and partly-fixed second primer, both having a sequence of randomized
PT   nucleotides.
XX
PS   Disclosure; Fig 2; 52pp; English.
XX
CC   The present invention relates to a method for amplifying a region of
CC   nucleic acid from a sample via PCR using several primers. The primers of
CC   the present invention have a region of fixed nucleotide sequence
CC   identical or complementary to a consensus sequence of interest and also
CC   have a region of randomised nucleotide sequence. The present sequence is
CC   the 3' splice junction consensus sequence, which was used to design PCR
CC   primers for use in the present invention. The method is useful for
CC   specifically amplifying a desired region of a nucleic acid, especially
CC   exons from a sample of DNA. The method is also applicable for amplifying
CC   regions flanking a consensus sequence in a sample of nucleic acid of
CC   totally or partially unknown sequence
XX
SQ   Sequence 15 BP; 1 A; 0 C; 2 G; 3 T; 0 U; 9 Other;

  Query Match             30.0%;  Score 3;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         10 RRR 8


RESULT 195
ADF29171
ID   ADF29171 standard; RNA; 15 BP.
XX
AC   ADF29171;
XX
DT   12-FEB-2004  (revised)
DT   18-SEP-2003  (first entry)
XX
DE   Beta-globin stabilising RNA motif.
XX
KW   tumour antigen; cancer; beta-globin; cytokine; RNase inhibitor; RNasin;
KW   vaccine; cytostatic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    5
FT                   /*tag=  a
FT                   /note= "Can be repeated n times where n is an undisclosed
FT                   figure"
FT   misc_feature    10
FT                   /*tag=  b
FT                   /note= "Can be repeated n times where n is an undisclosed
FT                   figure"
XX
PN   WO2003051401-A2.
XX
PD   26-JUN-2003.
XX
PF   19-DEC-2002; 2002WO-EP014577.
XX
PR   19-DEC-2001; 2001DE-01062480.
XX
PA   (CURE-) CUREVAC GMBH.
XX
PI   Hoerr I,  Von Der Muelbe F,  Pascolo S;
XX
DR   WPI; 2003-505463/47.
XX
PT   Composition containing mRNA encoding tumor antigen, useful as vaccine for
PT   treating and preventing tumors, particularly where mRNA is stabilized.
XX
PS   Claim 4; Page 10; 75pp; German.
XX
CC   This invention describes a novel pharmaceutical composition which
CC   contains at least one polynucleotide, including at least one region that
CC   encodes a tumour antigen and an aqueous solvent and is used for treatment
CC   and prevention of cancer. The polynucleotide, the antigen-encoding region
CC   and/or the 5' and/or 3'-untranslated regions are modified, relative to
CC   the wild type, to eliminate destabilising sequences. Preferably the
CC   polynucleotide has a 5'-cap structure and/or a polyA tail of at least 25
CC   nucleotides, at least one internal ribosome binding site and/or at least
CC   5' and/or 3'-stabilising sequences. Preferably the stabilising sequences
CC   are untranslated regions of the beta-globin gene or a sequence of formula
CC   (C/U)CCAN x CCC(U/A)Py x UC(C/U)CC. The polynucleotide may also (i)
CC   encode a cytokine or (ii) include a sequence that increases the
CC   transcription rate and is complexed, or condensed, with a (poly)cationic
CC   compound, e.g. protamine, poly(Lys or Arg) or histone. The composition
CC   may include (i) an RNase inhibitor, especially RNasin or (ii) many
CC   different nucleic acids, representing part of a cDNA library that encodes
CC   tumour-specific antigens. RNA avoids problems associated with use of DNA,
CC   e.g. integration into the genome; risk of viral recombination and
CC   induction of anti-DNA antibodies, but is normally too unstable for
CC   practical use. When stabilized, e.g. by incorporation of stabilizing
CC   sequences or non-natural nucleotides, it provides an effective vaccine.
CC   The products of the invention have cytostatic activity. This sequence
CC   represents a sequence stabilising motif described in the disclosure of
CC   the invention.
XX
SQ   Sequence 15 BP; 1 A; 8 C; 0 G; 0 T; 1 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          4 CWW 6
              |||
Db          8 CWW 10


RESULT 196
ADF29171/c
ID   ADF29171 standard; RNA; 15 BP.
XX
AC   ADF29171;
XX
DT   12-FEB-2004  (revised)
DT   18-SEP-2003  (first entry)
XX
DE   Beta-globin stabilising RNA motif.
XX
KW   tumour antigen; cancer; beta-globin; cytokine; RNase inhibitor; RNasin;
KW   vaccine; cytostatic; ss.
XX
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    5
FT                   /*tag=  a
FT                   /note= "Can be repeated n times where n is an undisclosed
FT                   figure"
FT   misc_feature    10
FT                   /*tag=  b
FT                   /note= "Can be repeated n times where n is an undisclosed
FT                   figure"
XX
PN   WO2003051401-A2.
XX
PD   26-JUN-2003.
XX
PF   19-DEC-2002; 2002WO-EP014577.
XX
PR   19-DEC-2001; 2001DE-01062480.
XX
PA   (CURE-) CUREVAC GMBH.
XX
PI   Hoerr I,  Von Der Muelbe F,  Pascolo S;
XX
DR   WPI; 2003-505463/47.
XX
PT   Composition containing mRNA encoding tumor antigen, useful as vaccine for
PT   treating and preventing tumors, particularly where mRNA is stabilized.
XX
PS   Claim 4; Page 10; 75pp; German.
XX
CC   This invention describes a novel pharmaceutical composition which
CC   contains at least one polynucleotide, including at least one region that
CC   encodes a tumour antigen and an aqueous solvent and is used for treatment
CC   and prevention of cancer. The polynucleotide, the antigen-encoding region
CC   and/or the 5' and/or 3'-untranslated regions are modified, relative to
CC   the wild type, to eliminate destabilising sequences. Preferably the
CC   polynucleotide has a 5'-cap structure and/or a polyA tail of at least 25
CC   nucleotides, at least one internal ribosome binding site and/or at least
CC   5' and/or 3'-stabilising sequences. Preferably the stabilising sequences
CC   are untranslated regions of the beta-globin gene or a sequence of formula
CC   (C/U)CCAN x CCC(U/A)Py x UC(C/U)CC. The polynucleotide may also (i)
CC   encode a cytokine or (ii) include a sequence that increases the
CC   transcription rate and is complexed, or condensed, with a (poly)cationic
CC   compound, e.g. protamine, poly(Lys or Arg) or histone. The composition
CC   may include (i) an RNase inhibitor, especially RNasin or (ii) many
CC   different nucleic acids, representing part of a cDNA library that encodes
CC   tumour-specific antigens. RNA avoids problems associated with use of DNA,
CC   e.g. integration into the genome; risk of viral recombination and
CC   induction of anti-DNA antibodies, but is normally too unstable for
CC   practical use. When stabilized, e.g. by incorporation of stabilizing
CC   sequences or non-natural nucleotides, it provides an effective vaccine.
CC   The products of the invention have cytostatic activity. This sequence
CC   represents a sequence stabilising motif described in the disclosure of
CC   the invention.
XX
SQ   Sequence 15 BP; 1 A; 8 C; 0 G; 0 T; 1 U; 5 Other;

  Query Match             30.0%;  Score 3;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db         10 WWG 8


RESULT 197
ADF29180
ID   ADF29180 standard; DNA; 15 BP.
XX
AC   ADF29180;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Binding oligonucleotide DNA #4.
XX
KW   ss; library; specific-binding agent; activation; inhibition; primer.
XX
OS   Synthetic.
XX
PN   WO2003056034-A2.
XX
PD   10-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-EP014584.
XX
PR   24-DEC-2001; 2001DE-01063986.
PR   09-FEB-2002; 2002DE-01005423.
PR   11-FEB-2002; 2002DE-01005571.
XX
PA   (NANO-) NANOTYPE GMBH.
XX
PI   Steipe B,  Clausen-Schaumann H,  Oesterhelt F;
XX
DR   WPI; 2003-569459/53.
XX
PT   In vitro selection of specific binding agents, useful potentially as
PT   pharmaceuticals and diagnostic agents, discriminates again non-specific,
PT   high-affinity agents.
XX
PS   Disclosure; Fig 7; 58pp; German.
XX
CC   This invention describes a novel in vitro method for selecting agents,
CC   present in a library of molecules, that bind to a target molecule. The
CC   method comprises first immobilizing the target molecules and contacting
CC   them with many molecules, which are bound to a reference complex so that
CC   the target molecule can bind to appropriate agents, forming a link of
CC   structure reference complex-agent-target molecule. Non-bound components
CC   are separated and a force is applied to the link so that one bond in it
CC   is broken, and the target molecule-bound agent, or its complement, is
CC   identified and/or amplified. The reference complex has a binding strength
CC   chosen to be smaller than that of a specifically bound agent, when a
CC   tractive force is applied. The method is used to select specific-binding
CC   agents, potentially useful as pharmaceuticals, e.g. for activation or
CC   inhibition of targets, also for diagnosis. High-affinity but non-specific
CC   binders are not selected, rather only those with specific binding,
CC   including any present only rarely in the test population, since selection
CC   is made without reaching thermodynamic equilibrium. This results in rapid
CC   selection and does not require stringent conditions, i.e. selection
CC   conditions are similar to physiological conditions. This sequence
CC   represents an oligonucleotide used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 15 BP; 7 A; 0 C; 0 G; 0 T; 0 U; 8 Other;
```

```
  Query Match             30.0%;  Score 3;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db          8 RRR 10


RESULT 198
ADF29180/c
ID   ADF29180 standard; DNA; 15 BP.
XX
AC   ADF29180;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Binding oligonucleotide DNA #4.
XX
KW   ss; library; specific-binding agent; activation; inhibition; primer.
XX
OS   Synthetic.
XX
PN   WO2003056034-A2.
XX
PD   10-JUL-2003.
XX
PF   19-DEC-2002; 2002WO-EP014584.
XX
PR   24-DEC-2001; 2001DE-01063986.
PR   09-FEB-2002; 2002DE-01005423.
PR   11-FEB-2002; 2002DE-01005571.
XX
PA   (NANO-) NANOTYPE GMBH.
XX
PI   Steipe B,  Clausen-Schaumann H,  Oesterhelt F;
XX
DR   WPI; 2003-569459/53.
XX
PT   In vitro selection of specific binding agents, useful potentially as
PT   pharmaceuticals and diagnostic agents, discriminates again non-specific,
PT   high-affinity agents.
XX
PS   Disclosure; Fig 7; 58pp; German.
XX
CC   This invention describes a novel in vitro method for selecting agents,
CC   present in a library of molecules, that bind to a target molecule. The
CC   method comprises first immobilizing the target molecules and contacting
CC   them with many molecules, which are bound to a reference complex so that
CC   the target molecule can bind to appropriate agents, forming a link of
CC   structure reference complex-agent-target molecule. Non-bound components
CC   are separated and a force is applied to the link so that one bond in it
CC   is broken, and the target molecule-bound agent, or its complement, is
CC   identified and/or amplified. The reference complex has a binding strength
CC   chosen to be smaller than that of a specifically bound agent, when a
CC   tractive force is applied. The method is used to select specific-binding
CC   agents, potentially useful as pharmaceuticals, e.g. for activation or
CC   inhibition of targets, also for diagnosis. High-affinity but non-specific
CC   binders are not selected, rather only those with specific binding,
CC   including any present only rarely in the test population, since selection
CC   is made without reaching thermodynamic equilibrium. This results in rapid
CC   selection and does not require stringent conditions, i.e. selection
CC   conditions are similar to physiological conditions. This sequence
CC   represents an oligonucleotide used to illustrate the method of the
CC   invention.
XX
SQ   Sequence 15 BP; 7 A; 0 C; 0 G; 0 T; 0 U; 8 Other;

  Query Match             30.0%;  Score 3;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db          15 YYY 13


RESULT 199
ADJ71750
ID   ADJ71750 standard; DNA; 15 BP.
XX
AC   ADJ71750;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Aptamer peptide display library generic insert.
XX
KW   cytostatic; analgesic; anticonvulsant; cerebroprotective;
KW   antiparkinsonian; nootropic; neuroprotective; anti-HIV;
KW   modulator of cell phenotype; gene therapy; peptide aptamer;
KW   cell phenotype modification; peptide display library; cancer; pain;
KW   epilepsy; stroke; Parkinson's disease; Alzheimer's disease;
KW   Huntington's disease; multiple sclerosis; AIDS; ds; gene; ss.
XX
OS   Synthetic.
XX
PN   WO2003040168-A2.
XX
PD   15-MAY-2003.
XX
PF   06-NOV-2002; 2002WO-US035584.
XX
PR   06-NOV-2001; 2001US-0333262P.
PR   14-FEB-2002; 2002US-0357278P.
XX
PA   (ENAN-) ENANTA PHARM INC.
XX
PI   Benson JD,  Vincent SM,  Brasher BB,  Miao Z,  Lamming D;
XX
DR   WPI; 2003-541418/51.
XX
PT   Identifying peptide aptamer capable of modifying cell phenotype, by
PT   contacting cell sample with library encoding random peptide aptamers,
PT   selecting cell with altered phenotype, and identifying aptamers expressed
PT   in cell.
XX
PS   Example 1; SEQ ID NO 6; 173pp; English.
XX
CC   The invention relates to a method of identifying (M1) a peptide aptamer
CC   (PA) capable of modifying a cell phenotype, involving contacting a 1st
CC   sample of cells with a library of expressible nucleic acid sequences
CC   encoding random peptide aptamers linked to a fusion moiety, selecting at
CC   least one cell having an altered phenotype compared to the phenotype of
CC   the cell prior to contacting, and identifying peptide aptamers expressed
CC   in the selected cell. PA, its derivative or corresponding nucleic acid is
CC   useful for the molecular modelling of an agent having similar binding
CC   characteristics as PA. PA, its derivative or corresponding expressible
CC   nucleic acid is useful for treating or inhibiting a disease or condition
CC   (such as cancer) associated with an aberrant cell phenotype in a subject,
CC   where the aberrant cell phenotype is associated with a change in levels
CC   of apoptosis, viral resistance, signal transduction, protein trafficking,
CC   cell adhesion, membrane transport, cell motility, metabolic state or
CC   differentiation, when compared to a control cell, or the aberrant cell
CC   phenotype is associated with a tumor cell. The expressible nucleic acid
CC   is administered using a retrovirus that comprises a chromatin insulator
CC   element. PA is useful as a prognostic or diagnostic tool, for altering a
CC   cell phenotype, in gene therapy, as therapeutics for treating diseases
CC   (such as pain, epilepsy, stroke, Parkinson's disease, Alzheimer's
CC   disease, Huntington's disease, multiple sclerosis, AIDS), and for the
CC   research and development of other therapeutics. This sequence represents
CC   the generic sequence used to generate the peptide display library (in
CC   retroviruses) and used to generate the aptamers of the invention.
XX
SQ   Sequence 15 BP; 3 A; 0 C; 1 G; 4 T; 0 U; 7 Other;

  Query Match             30.0%;  Score 3;  DB 10;  Length 15;
```

```
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYY 9
              |||
Db         11 GYY 13


RESULT 200
ADJ71750/c
ID   ADJ71750 standard; DNA; 15 BP.
XX
AC   ADJ71750;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Aptamer peptide display library generic insert.
XX
KW   cytostatic; analgesic; anticonvulsant; cerebroprotective;
KW   antiparkinsonian; nootropic; neuroprotective; anti-HIV;
KW   modulator of cell phenotype; gene therapy; peptide aptamer;
KW   cell phenotype modification; peptide display library; cancer; pain;
KW   epilepsy; stroke; Parkinson's disease; Alzheimer's disease;
KW   Huntington's disease; multiple sclerosis; AIDS; ds; gene; ss.
XX
OS   Synthetic.
XX
PN   WO2003040168-A2.
XX
PD   15-MAY-2003.
XX
PF   06-NOV-2002; 2002WO-US035584.
XX
PR   06-NOV-2001; 2001US-0333262P.
PR   14-FEB-2002; 2002US-0357278P.
XX
PA   (ENAN-) ENANTA PHARM INC.
XX
PI   Benson JD,  Vincent SM,  Brasher BB,  Miao Z,  Lamming D;
XX
DR   WPI; 2003-541418/51.
XX
PT   Identifying peptide aptamer capable of modifying cell phenotype, by
PT   contacting cell sample with library encoding random peptide aptamers,
PT   selecting cell with altered phenotype, and identifying aptamers expressed
PT   in cell.
XX
PS   Example 1; SEQ ID NO 6; 173pp; English.
XX
CC   The invention relates to a method of identifying (M1) a peptide aptamer
CC   (PA) capable of modifying a cell phenotype, involving contacting a 1st
CC   sample of cells with a library of expressible nucleic acid sequences
CC   encoding random peptide aptamers linked to a fusion moiety, selecting at
CC   least one cell having an altered phenotype compared to the phenotype of
CC   the cell prior to contacting, and identifying peptide aptamers expressed
CC   in the selected cell. PA, its derivative or corresponding nucleic acid is
CC   useful for the molecular modelling of an agent having similar binding
CC   characteristics as PA. PA, its derivative or corresponding expressible
CC   nucleic acid is useful for treating or inhibiting a disease or condition
CC   (such as cancer) associated with an aberrant cell phenotype in a subject,
CC   where the aberrant cell phenotype is associated with a change in levels
CC   of apoptosis, viral resistance, signal transduction, protein trafficking,
CC   cell adhesion, membrane transport, cell motility, metabolic state or
CC   differentiation, when compared to a control cell, or the aberrant cell
CC   phenotype is associated with a tumor cell. The expressible nucleic acid
CC   is administered using a retrovirus that comprises a chromatin insulator
CC   element. PA is useful as a prognostic or diagnostic tool, for altering a
CC   cell phenotype, in gene therapy, as therapeutics for treating diseases
CC   (such as pain, epilepsy, stroke, Parkinson's disease, Alzheimer's
CC   disease, Huntington's disease, multiple sclerosis, AIDS), and for the
CC   research and development of other therapeutics. This sequence represents
CC   the generic sequence used to generate the peptide display library (in
CC   retroviruses) and used to generate the aptamers of the invention.
XX
SQ   Sequence 15 BP; 3 A; 0 C; 1 G; 4 T; 0 U; 7 Other;

  Query Match             30.0%;  Score 3;  DB 10;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db         13 RRC 11


Search completed: January 14, 2005, 16:40:02
Job time : 409 secs
```

OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 16:22:09 ; Search time 2717 Seconds
(without alignments)
134.118 Million cell updates/sec

Title: US-09-813-824A-3
Perfect score: 10
Sequence: 1 RRRCWWGYYY 10

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 32822875 seqs, 18219865908 residues

Word size : 0

Total number of hits satisfying chosen parameters: 664238

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 1000 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	4	40.0	74	9	CNS015BQ	AL105248 Drosophil
c	2	4	40.0	74	9	CNS015BQ	AL105248 Drosophil
	3	4	40.0	77	1	AF211608	AF211608 AF211608
c	4	4	40.0	77	1	AF211608	AF211608 AF211608
	5	3	30.0	63	3	AY431131	AY431131 Aedes aeg
c	6	3	30.0	63	3	AY431131	AY431131 Aedes aeg
	7	3	30.0	68	9	CNS011MQ	AL100460 Drosophil
c	8	3	30.0	68	9	CNS011MQ	AL100460 Drosophil
	9	3	30.0	70	7	T24836	T24836 EST411 Huma
c	10	3	30.0	70	7	T24836	T24836 EST411 Huma
	11	3	30.0	88	1	AJ283222	AJ283222 4A3A-P8D3
c	12	3	30.0	88	1	AJ283222	AJ283222 4A3A-P8D3
	13	3	30.0	90	7	T24971	T24971 EST546 Huma
c	14	3	30.0	90	7	T24971	T24971 EST546 Huma
	15	3	30.0	91	5	BQ704626	BQ704626 Bn01_0312
c	16	3	30.0	91	5	BQ704626	BQ704626 Bn01_0312
	17	3	30.0	92	3	AY431374	AY431374 Aedes aeg
c	18	3	30.0	92	3	AY431374	AY431374 Aedes aeg
	19	3	30.0	93	9	CNS00YZ0	AL097014 Drosophil
c	20	3	30.0	93	9	CNS00YZ0	AL097014 Drosophil
	21	3	30.0	96	9	CNS0107O	AL098622 Drosophil
c	22	3	30.0	96	9	CNS0107O	AL098622 Drosophil
	23	3	30.0	98	9	CNS0429N	AL271220 Tetraodon
c	24	3	30.0	98	9	CNS0429N	AL271220 Tetraodon
	25	2	20.0	25	9	CNS00I17	AL074604 Drosophil
c	26	2	20.0	25	9	CNS00I17	AL074604 Drosophil
	27	2	20.0	30	9	CNS00C45	AL058402 Drosophil
c	28	2	20.0	30	9	CNS00C45	AL058402 Drosophil
	29	2	20.0	36	9	CNS00JBW	AL075982 Drosophil
c	30	2	20.0	36	9	CNS00JBW	AL075982 Drosophil
	31	2	20.0	38	9	CNS00L8C	AL068197 Drosophil
c	32	2	20.0	38	9	CNS00L8C	AL068197 Drosophil
	33	2	20.0	41	2	AW059591	AW059591 HuTH.bsst
c	34	2	20.0	41	2	AW059591	AW059591 HuTH.bsst
	35	2	20.0	41	2	AW059842	AW059842 HuTH.bsst
c	36	2	20.0	41	2	AW059842	AW059842 HuTH.bsst
	37	2	20.0	41	2	AW059847	AW059847 HuTH.bsst
c	38	2	20.0	41	2	AW059847	AW059847 HuTH.bsst
	39	2	20.0	41	9	CNS00COP	AL059445 Drosophil
c	40	2	20.0	41	9	CNS00COP	AL059445 Drosophil
	41	2	20.0	43	9	CNS00COG	AL059436 Drosophil
c	42	2	20.0	43	9	CNS00COG	AL059436 Drosophil
	43	2	20.0	45	7	CN813621	CN813621 Fg06_0210
c	44	2	20.0	45	7	CN813621	CN813621 Fg06_0210
	45	2	20.0	47	2	AW059540	AW059540 HuTH.bsst
c	46	2	20.0	47	2	AW059540	AW059540 HuTH.bsst
	47	2	20.0	48	9	CNS00J6U	AL075800 Drosophil
c	48	2	20.0	48	9	CNS00J6U	AL075800 Drosophil
	49	2	20.0	49	2	AW496816	AW496816 1cj Neuro
c	50	2	20.0	49	2	AW496816	AW496816 1cj Neuro
	51	2	20.0	50	9	CNS00AWB	AL056017 Drosophil
c	52	2	20.0	50	9	CNS00AWB	AL056017 Drosophil
	53	2	20.0	51	2	AW444398	AW444398 AB558 Pri
c	54	2	20.0	51	2	AW444398	AW444398 AB558 Pri
	55	2	20.0	51	9	CNS00BFG	AL057009 Drosophil
c	56	2	20.0	51	9	CNS00BFG	AL057009 Drosophil
	57	2	20.0	51	9	CNS00IH3	AL074772 Drosophil
c	58	2	20.0	51	9	CNS00IH3	AL074772 Drosophil
	59	2	20.0	51	9	CNS02CBU	AL190947 Tetraodon
c	60	2	20.0	51	9	CNS02CBU	AL190947 Tetraodon
	61	2	20.0	52	2	AW582795	AW582795 1sm Neuro
c	62	2	20.0	52	2	AW582795	AW582795 1sm Neuro
	63	2	20.0	52	9	CNS0102A	AL098428 Drosophil
c	64	2	20.0	52	9	CNS0102A	AL098428 Drosophil
	65	2	20.0	52	9	CNS011OZ	AL100541 Drosophil
c	66	2	20.0	52	9	CNS011OZ	AL100541 Drosophil
	67	2	20.0	52	9	CNS011VR	AL100785 Drosophil
c	68	2	20.0	52	9	CNS011VR	AL100785 Drosophil
	69	2	20.0	53	3	AY432321	AY432321 Aedes aeg
c	70	2	20.0	53	3	AY432321	AY432321 Aedes aeg
	71	2	20.0	53	3	AY440477	AY440477 Armigeres
c	72	2	20.0	53	3	AY440477	AY440477 Armigeres
	73	2	20.0	53	9	CNS02YBO	AL219453 Tetraodon
c	74	2	20.0	53	9	CNS02YBO	AL219453 Tetraodon
	75	2	20.0	54	3	AY431290	AY431290 Aedes aeg
c	76	2	20.0	54	3	AY431290	AY431290 Aedes aeg
	77	2	20.0	55	2	AW497627	AW497627 rps7g2b81
c	78	2	20.0	55	2	AW497627	AW497627 rps7g2b81
	79	2	20.0	55	9	CNS025NE	AL182291 Tetraodon
c	80	2	20.0	55	9	CNS025NE	AL182291 Tetraodon
	81	2	20.0	56	2	AW444238	AW444238 AB562 Bas
c	82	2	20.0	56	2	AW444238	AW444238 AB562 Bas
	83	2	20.0	56	2	AW444409	AW444409 AB573 Pri
c	84	2	20.0	56	2	AW444409	AW444409 AB573 Pri
	85	2	20.0	56	4	BG838323	BG838323 Gc01_08e0
c	86	2	20.0	56	4	BG838323	BG838323 Gc01_08e0
	87	2	20.0	56	9	CNS013GI	AL102828 Drosophil
c	88	2	20.0	56	9	CNS013GI	AL102828 Drosophil
	89	2	20.0	57	9	CNS00BH8	AL057073 Drosophil
c	90	2	20.0	57	9	CNS00BH8	AL057073 Drosophil
	91	2	20.0	57	9	CNS0217V	AL176548 Tetraodon
c	92	2	20.0	57	9	CNS0217V	AL176548 Tetraodon
	93	2	20.0	57	9	CNS02S8W	AL211577 Tetraodon
c	94	2	20.0	57	9	CNS02S8W	AL211577 Tetraodon
	95	2	20.0	57	9	CNS03R92	AL256943 Tetraodon
c	96	2	20.0	57	9	CNS03R92	AL256943 Tetraodon
	97	2	20.0	58	3	AY439683	AY439683 Armigeres

c	98	2	20.0	58	3	AY439683	AY439683	Armigeres		171	2	20.0	62	9	CNS0119R	AL099993	Drosophil
	99	2	20.0	59	1	AF211549	AF211549		c	172	2	20.0	62	9	CNS0119R	AL099993	Drosophil
c	100	2	20.0	59	1	AF211549	AF211549			173	2	20.0	62	9	CNS02QCA	AL209107	Tetraodon
	101	2	20.0	59	3	AY439538	AY439538	Armigeres	c	174	2	20.0	62	9	CNS02QCA	AL209107	Tetraodon
c	102	2	20.0	59	3	AY439538	AY439538	Armigeres		175	2	20.0	62	9	CNS04A3J	AL281368	Tetraodon
	103	2	20.0	59	9	CNS0111A	AL099688	Drosophil	c	176	2	20.0	62	9	CNS04A3J	AL281368	Tetraodon
c	104	2	20.0	59	9	CNS0111A	AL099688	Drosophil		177	2	20.0	63	2	AW444235	AW444235	AB555 Bas
	105	2	20.0	59	9	CNS014IM	AL104200	Drosophil	c	178	2	20.0	63	2	AW444235	AW444235	AB555 Bas
c	106	2	20.0	59	9	CNS014IM	AL104200	Drosophil		179	2	20.0	63	2	AW444251	AW444251	AB015 Pri
	107	2	20.0	60	2	AW059629	AW059629	HuTH.bsst	c	180	2	20.0	63	2	AW444251	AW444251	AB015 Pri
c	108	2	20.0	60	2	AW059629	AW059629	HuTH.bsst		181	2	20.0	63	3	AY440539	AY440539	Armigeres
	109	2	20.0	60	2	AW582843	AW582843	top3g66 N	c	182	2	20.0	63	3	AY440539	AY440539	Armigeres
c	110	2	20.0	60	2	AW582843	AW582843	top3g66 N		183	2	20.0	63	4	BG838614	BG838614	Gc01_05d0
	111	2	20.0	60	3	AY432469	AY432469	Aedes aeg	c	184	2	20.0	63	4	BG838614	BG838614	Gc01_05d0
c	112	2	20.0	60	3	AY432469	AY432469	Aedes aeg		185	2	20.0	63	9	CNS017GA	AL108004	Drosophil
	113	2	20.0	60	3	AY432601	AY432601	Aedes aeg	c	186	2	20.0	63	9	CNS017GA	AL108004	Drosophil
c	114	2	20.0	60	3	AY432601	AY432601	Aedes aeg		187	2	20.0	63	9	CNS01VCH	AL168938	Tetraodon
	115	2	20.0	60	9	CNS00ARA	AL055937	Drosophil	c	188	2	20.0	63	9	CNS01VCH	AL168938	Tetraodon
c	116	2	20.0	60	9	CNS00ARA	AL055937	Drosophil		189	2	20.0	63	9	CNS02JW3	AL200748	Tetraodon
	117	2	20.0	60	9	CNS010IK	AL099014	Drosophil	c	190	2	20.0	63	9	CNS02JW3	AL200748	Tetraodon
c	118	2	20.0	60	9	CNS010IK	AL099014	Drosophil		191	2	20.0	63	9	CNS02PAK	AL207749	Tetraodon
	119	2	20.0	60	9	CNS0115W	AL099854	Drosophil	c	192	2	20.0	63	9	CNS02PAK	AL207749	Tetraodon
c	120	2	20.0	60	9	CNS0115W	AL099854	Drosophil		193	2	20.0	63	9	CNS03SXE	AL259115	Tetraodon
	121	2	20.0	60	9	CNS01TCC	AL166341	Tetraodon	c	194	2	20.0	63	9	CNS03SXE	AL259115	Tetraodon
c	122	2	20.0	60	9	CNS01TCC	AL166341	Tetraodon		195	2	20.0	63	9	CNS04DE2	AL285635	Tetraodon
	123	2	20.0	60	9	CNS028B0	AL185733	Tetraodon	c	196	2	20.0	63	9	CNS04DE2	AL285635	Tetraodon
c	124	2	20.0	60	9	CNS028B0	AL185733	Tetraodon		197	2	20.0	64	7	R28845	R28845	F1-6D 22 we
	125	2	20.0	60	9	CNS02K40	AL201033	Tetraodon	c	198	2	20.0	64	7	R28845	R28845	F1-6D 22 we
c	126	2	20.0	60	9	CNS02K40	AL201033	Tetraodon		199	2	20.0	64	9	CNS00DAF	AL060631	Drosophil
	127	2	20.0	60	9	CNS02OIW	AL206753	Tetraodon	c	200	2	20.0	64	9	CNS00DAF	AL060631	Drosophil
c	128	2	20.0	60	9	CNS02OIW	AL206753	Tetraodon		201	2	20.0	64	9	CNS011Z2	AL100904	Drosophil
	129	2	20.0	60	9	CNS0330M	AL225535	Tetraodon	c	202	2	20.0	64	9	CNS011Z2	AL100904	Drosophil
c	130	2	20.0	60	9	CNS0330M	AL225535	Tetraodon		203	2	20.0	64	9	CNS016S2	AL107132	Drosophil
	131	2	20.0	60	9	CNS03C5T	AL237386	Tetraodon	c	204	2	20.0	64	9	CNS016S2	AL107132	Drosophil
c	132	2	20.0	60	9	CNS03C5T	AL237386	Tetraodon		205	2	20.0	64	9	CNS01WJY	AL170503	Tetraodon
	133	2	20.0	60	9	CNS03QDZ	AL255824	Tetraodon	c	206	2	20.0	64	9	CNS01WJY	AL170503	Tetraodon
c	134	2	20.0	60	9	CNS03QDZ	AL255824	Tetraodon		207	2	20.0	64	9	CNS0263F	AL182868	Tetraodon
	135	2	20.0	61	3	AY431565	AY431565	Aedes aeg	c	208	2	20.0	64	9	CNS0263F	AL182868	Tetraodon
c	136	2	20.0	61	3	AY431565	AY431565	Aedes aeg		209	2	20.0	64	9	CNS02D0I	AL191835	Tetraodon
	137	2	20.0	61	3	AY432562	AY432562	Aedes aeg	c	210	2	20.0	64	9	CNS02D0I	AL191835	Tetraodon
c	138	2	20.0	61	3	AY432562	AY432562	Aedes aeg		211	2	20.0	64	9	CNS03NRA	AL252415	Tetraodon
	139	2	20.0	61	3	AY432871	AY432871	Aedes aeg	c	212	2	20.0	64	9	CNS03NRA	AL252415	Tetraodon
c	140	2	20.0	61	3	AY432871	AY432871	Aedes aeg		213	2	20.0	65	2	AW444213	AW444213	AB501 Bas
	141	2	20.0	61	7	L76124	L76124	SCMRAP0218	c	214	2	20.0	65	2	AW444213	AW444213	AB501 Bas
c	142	2	20.0	61	7	L76124	L76124	SCMRAP0218		215	2	20.0	65	3	AY439824	AY439824	Armigeres
	143	2	20.0	61	9	CNS0139J	AL102577	Drosophil	c	216	2	20.0	65	3	AY439824	AY439824	Armigeres
c	144	2	20.0	61	9	CNS0139J	AL102577	Drosophil		217	2	20.0	65	9	CNS03NIN	AL252104	Tetraodon
	145	2	20.0	61	9	CNS02J97	AL199924	Tetraodon	c	218	2	20.0	65	9	CNS03NIN	AL252104	Tetraodon
c	146	2	20.0	61	9	CNS02J97	AL199924	Tetraodon		219	2	20.0	66	1	AF211756	AF211756	AF211756
	147	2	20.0	61	9	CNS02MP4	AL204385	Tetraodon	c	220	2	20.0	66	1	AF211756	AF211756	
c	148	2	20.0	61	9	CNS02MP4	AL204385	Tetraodon		221	2	20.0	66	2	AW444305	AW444305	AB229 Pri
	149	2	20.0	61	9	CNS03955	AL233474	Tetraodon	c	222	2	20.0	66	2	AW444305	AW444305	AB229 Pri
c	150	2	20.0	61	9	CNS03955	AL233474	Tetraodon		223	2	20.0	66	3	AY432740	AY432740	Aedes aeg
	151	2	20.0	61	9	CNS03UDP	AL260998	Tetraodon	c	224	2	20.0	66	3	AY432740	AY432740	Aedes aeg
c	152	2	20.0	61	9	CNS03UDP	AL260998	Tetraodon		225	2	20.0	66	7	L76130	L76130	SCMRAP0224
	153	2	20.0	61	9	CNS044FV	AL274036	Tetraodon	c	226	2	20.0	66	7	L76130	L76130	SCMRAP0224
c	154	2	20.0	61	9	CNS044FV	AL274036	Tetraodon		227	2	20.0	66	9	CNS00GR8	AL072444	Drosophil
	155	2	20.0	62	2	AW059587	AW059587	HuTH.bsst	c	228	2	20.0	66	9	CNS00GR8	AL072444	Drosophil
c	156	2	20.0	62	2	AW059587	AW059587	HuTH.bsst		229	2	20.0	66	9	CNS00ZKP	AL097795	Drosophil
	157	2	20.0	62	2	AW059628	AW059628	HuTH.bsst	c	230	2	20.0	66	9	CNS00ZKP	AL097795	Drosophil
c	158	2	20.0	62	2	AW059628	AW059628	HuTH.bsst		231	2	20.0	66	9	CNS0212N	AL176360	Tetraodon
	159	2	20.0	62	2	BE577741	BE577741	EST011 Pi	c	232	2	20.0	66	9	CNS0212N	AL176360	Tetraodon
c	160	2	20.0	62	2	BE577741	BE577741	EST011 Pi		233	2	20.0	66	9	CNS045GR	AL275364	Tetraodon
	161	2	20.0	62	3	AY433080	AY433080	Aedes aeg	c	234	2	20.0	66	9	CNS045GR	AL275364	Tetraodon
c	162	2	20.0	62	3	AY433080	AY433080	Aedes aeg		235	2	20.0	67	2	AW444171	AW444171	AB308 Bas
	163	2	20.0	62	3	AY440494	AY440494	Armigeres	c	236	2	20.0	67	2	AW444171	AW444171	AB308 Bas
c	164	2	20.0	62	3	AY440494	AY440494	Armigeres		237	2	20.0	67	9	CNS00AGZ	AL055768	Drosophil
	165	2	20.0	62	5	BQ704656	BQ704656	Bn01_03h2	c	238	2	20.0	67	9	CNS00AGZ	AL055768	Drosophil
c	166	2	20.0	62	5	BQ704656	BQ704656	Bn01_03h2		239	2	20.0	67	9	CNS00BRW	AL057558	Drosophil
	167	2	20.0	62	9	CNS00CEZ	AL058792	Drosophil	c	240	2	20.0	67	9	CNS00BRW	AL057558	Drosophil
c	168	2	20.0	62	9	CNS00CEZ	AL058792	Drosophil		241	2	20.0	67	9	CNS011DR	AL100137	Drosophil
	169	2	20.0	62	9	CNS00IGI	AL074751	Drosophil	c	242	2	20.0	67	9	CNS011DR	AL100137	Drosophil
c	170	2	20.0	62	9	CNS00IGI	AL074751	Drosophil		243	2	20.0	67	9	CNS01WQ8	AL170729	Tetraodon

c 244	2	20.0	67	9	CNS01WQ8	AL170729	Tetraodon
245	2	20.0	67	9	CNS02O5Z	AL206288	Tetraodon
c 246	2	20.0	67	9	CNS02O5Z	AL206288	Tetraodon
247	2	20.0	67	9	CNS02PU7	AL208456	Tetraodon
c 248	2	20.0	67	9	CNS02PU7	AL208456	Tetraodon
249	2	20.0	67	9	CNS0482T	AL278750	Tetraodon
c 250	2	20.0	67	9	CNS0482T	AL278750	Tetraodon
251	2	20.0	67	9	CNS04KAU	AL294591	Tetraodon
c 252	2	20.0	67	9	CNS04KAU	AL294591	Tetraodon
253	2	20.0	68	4	BG321688	BG321688	Ds01_02h0
c 254	2	20.0	68	4	BG321688	BG321688	Ds01_02h0
255	2	20.0	68	9	CNS00I0F	AL074576	Drosophil
c 256	2	20.0	68	9	CNS00I0F	AL074576	Drosophil
257	2	20.0	68	9	CNS0115R	AL099849	Drosophil
c 258	2	20.0	68	9	CNS0115R	AL099849	Drosophil
259	2	20.0	68	9	CNS011H7	AL100261	Drosophil
c 260	2	20.0	68	9	CNS011H7	AL100261	Drosophil
261	2	20.0	68	9	CNS011Q8	AL100586	Drosophil
c 262	2	20.0	68	9	CNS011Q8	AL100586	Drosophil
263	2	20.0	68	9	CNS0223B	AL177680	Tetraodon
c 264	2	20.0	68	9	CNS0223B	AL177680	Tetraodon
265	2	20.0	68	9	CNS02PGH	AL207962	Tetraodon
c 266	2	20.0	68	9	CNS02PGH	AL207962	Tetraodon
267	2	20.0	68	9	CNS033MR	AL226332	Tetraodon
c 268	2	20.0	68	9	CNS033MR	AL226332	Tetraodon
269	2	20.0	68	9	CNS04DLF	AL285900	Tetraodon
c 270	2	20.0	68	9	CNS04DLF	AL285900	Tetraodon
271	2	20.0	69	1	AF211775	AF211775	AF211775
c 272	2	20.0	69	1	AF211775	AF211775	
273	2	20.0	69	2	AW059623	AW059623	HuTH.bsst
c 274	2	20.0	69	2	AW059623	AW059623	HuTH.bsst
275	2	20.0	69	9	CNS012M7	AL101737	Drosophil
c 276	2	20.0	69	9	CNS012M7	AL101737	Drosophil
277	2	20.0	69	9	CNS015U2	AL105908	Drosophil
c 278	2	20.0	69	9	CNS015U2	AL105908	Drosophil
279	2	20.0	69	9	CNS0161X	AL106191	Drosophil
c 280	2	20.0	69	9	CNS0161X	AL106191	Drosophil
281	2	20.0	69	9	CNS01V0D	AL168502	Tetraodon
c 282	2	20.0	69	9	CNS01V0D	AL168502	Tetraodon
283	2	20.0	69	9	CNS03TJB	AL259904	Tetraodon
c 284	2	20.0	69	9	CNS03TJB	AL259904	Tetraodon
285	2	20.0	70	2	AW582796	AW582796	2zm Neuro
c 286	2	20.0	70	2	AW582796	AW582796	2zm Neuro
287	2	20.0	70	6	CD457769	CD457769	Fg04d_03o
c 288	2	20.0	70	6	CD457769	CD457769	Fg04d_03o
289	2	20.0	70	7	L76123	L76123	SCMRAP0217
c 290	2	20.0	70	7	L76123	L76123	SCMRAP0217
291	2	20.0	70	9	CNS01XV6	AL172203	Tetraodon
c 292	2	20.0	70	9	CNS01XV6	AL172203	Tetraodon
293	2	20.0	70	9	CNS02E3X	AL193254	Tetraodon
c 294	2	20.0	70	9	CNS02E3X	AL193254	Tetraodon
295	2	20.0	70	9	CNS0321F	AL224268	Tetraodon
c 296	2	20.0	70	9	CNS0321F	AL224268	Tetraodon
297	2	20.0	70	9	CNS04KX7	AL295396	Tetraodon
c 298	2	20.0	70	9	CNS04KX7	AL295396	Tetraodon
299	2	20.0	71	2	AW059584	AW059584	HuTH.bsst
c 300	2	20.0	71	2	AW059584	AW059584	HuTH.bsst
301	2	20.0	71	3	AY439626	AY439626	Armigeres
c 302	2	20.0	71	3	AY439626	AY439626	Armigeres
303	2	20.0	71	3	AY439798	AY439798	Armigeres
c 304	2	20.0	71	3	AY439798	AY439798	Armigeres
305	2	20.0	71	6	CD457700	CD457700	Fg04d_03a
c 306	2	20.0	71	6	CD457700	CD457700	Fg04d_03a
307	2	20.0	71	9	CNS00ZKZ	AL097805	Drosophil
c 308	2	20.0	71	9	CNS00ZKZ	AL097805	Drosophil
309	2	20.0	71	9	CNS011Z5	AL100907	Drosophil
c 310	2	20.0	71	9	CNS011Z5	AL100907	Drosophil
311	2	20.0	71	9	CNS01S4U	AL164775	Tetraodon
c 312	2	20.0	71	9	CNS01S4U	AL164775	Tetraodon
313	2	20.0	71	9	CNS03WAK	AL263477	Tetraodon
c 314	2	20.0	71	9	CNS03WAK	AL263477	Tetraodon
315	2	20.0	72	1	AF211718	AF211718	AF211718
c 316	2	20.0	72	1	AF211718	AF211718	AF211718
317	2	20.0	72	7	T24492	T24492	EST067 Huma
c 318	2	20.0	72	7	T24492	T24492	EST067 Huma
319	2	20.0	72	9	CNS013KD	AL102967	Drosophil
c 320	2	20.0	72	9	CNS013KD	AL102967	Drosophil
321	2	20.0	72	9	CNS02411	AL180190	Tetraodon
c 322	2	20.0	72	9	CNS02411	AL180190	Tetraodon
323	2	20.0	72	9	CNS03DWN	AL239648	Tetraodon
c 324	2	20.0	72	9	CNS03DWN	AL239648	Tetraodon
325	2	20.0	72	9	CNS04AOG	AL282121	Tetraodon
c 326	2	20.0	72	9	CNS04AOG	AL282121	Tetraodon
327	2	20.0	73	3	AY432861	AY432861	Aedes aeg
c 328	2	20.0	73	3	AY432861	AY432861	Aedes aeg
329	2	20.0	73	3	AY433262	AY433262	Aedes aeg
c 330	2	20.0	73	3	AY433262	AY433262	Aedes aeg
331	2	20.0	73	3	AY439747	AY439747	Armigeres
c 332	2	20.0	73	3	AY439747	AY439747	Armigeres
333	2	20.0	73	3	AY440001	AY440001	Armigeres
c 334	2	20.0	73	3	AY440001	AY440001	Armigeres
335	2	20.0	73	3	AY440687	AY440687	Armigeres
c 336	2	20.0	73	3	AY440687	AY440687	Armigeres
337	2	20.0	73	6	CD458545	CD458545	Fg08_11h1
c 338	2	20.0	73	6	CD458545	CD458545	Fg08_11h1
339	2	20.0	73	9	CNS008IX	AL052135	Drosophil
c 340	2	20.0	73	9	CNS008IX	AL052135	Drosophil
341	2	20.0	73	9	CNS00ZY1	AL098275	Drosophil
c 342	2	20.0	73	9	CNS00ZY1	AL098275	Drosophil
343	2	20.0	73	9	CNS0167O	AL106398	Drosophil
c 344	2	20.0	73	9	CNS0167O	AL106398	Drosophil
345	2	20.0	73	9	CNS02FGM	AL195007	Tetraodon
c 346	2	20.0	73	9	CNS02FGM	AL195007	Tetraodon
347	2	20.0	73	9	CNS03MDO	AL250629	Tetraodon
c 348	2	20.0	73	9	CNS03MDO	AL250629	Tetraodon
349	2	20.0	73	9	CNS04POB	AL301556	Tetraodon
c 350	2	20.0	73	9	CNS04POB	AL301556	Tetraodon
351	2	20.0	74	2	AW444240	AW444240	AB571 Bas
c 352	2	20.0	74	2	AW444240	AW444240	AB571 Bas
353	2	20.0	74	3	AY431853	AY431853	Aedes aeg
c 354	2	20.0	74	3	AY431853	AY431853	Aedes aeg
355	2	20.0	74	3	AY439801	AY439801	Armigeres
c 356	2	20.0	74	3	AY439801	AY439801	Armigeres
357	2	20.0	74	3	AY440440	AY440440	Armigeres
c 358	2	20.0	74	3	AY440440	AY440440	Armigeres
359	2	20.0	74	9	CNS020LX	AL175758	Tetraodon
c 360	2	20.0	74	9	CNS020LX	AL175758	Tetraodon
361	2	20.0	74	9	CNS02NIN	AL205448	Tetraodon
c 362	2	20.0	74	9	CNS02NIN	AL205448	Tetraodon
363	2	20.0	75	3	AY440583	AY440583	Armigeres
c 364	2	20.0	75	3	AY440583	AY440583	Armigeres
365	2	20.0	75	9	CNS00BGI	AL057047	Drosophil
c 366	2	20.0	75	9	CNS00BGI	AL057047	Drosophil
367	2	20.0	75	9	CNS00CHF	AL059284	Drosophil
c 368	2	20.0	75	9	CNS00CHF	AL059284	Drosophil
369	2	20.0	75	9	CNS03EB6	AL240171	Tetraodon
c 370	2	20.0	75	9	CNS03EB6	AL240171	Tetraodon
371	2	20.0	75	9	CNS048VA	AL279775	Tetraodon
c 372	2	20.0	75	9	CNS048VA	AL279775	Tetraodon
373	2	20.0	75	9	CNS06UIT	AL415899	T3 end of
c 374	2	20.0	75	9	CNS06UIT	AL415899	T3 end of
375	2	20.0	76	1	AF037644	AF037644	AF037644
c 376	2	20.0	76	1	AF037644	AF037644	AF037644
377	2	20.0	76	2	AW059546	AW059546	HuTH.bsst
c 378	2	20.0	76	2	AW059546	AW059546	HuTH.bsst
379	2	20.0	76	2	AW444223	AW444223	AB527 Bas
c 380	2	20.0	76	2	AW444223	AW444223	AB527 Bas
381	2	20.0	76	3	AY431930	AY431930	Aedes aeg
c 382	2	20.0	76	3	AY431930	AY431930	Aedes aeg
383	2	20.0	76	9	CNS004EH	AL051336	Drosophil
c 384	2	20.0	76	9	CNS004EH	AL051336	Drosophil
385	2	20.0	76	9	CNS02F53	AL194592	Tetraodon
c 386	2	20.0	76	9	CNS02F53	AL194592	Tetraodon
387	2	20.0	76	9	CNS03DSF	AL239496	Tetraodon
c 388	2	20.0	76	9	CNS03DSF	AL239496	Tetraodon
389	2	20.0	77	2	AW582791	AW582791	1mku Neur

c 390	2	20.0	77	2	AW582791	AW582791 1mku Neur
391	2	20.0	77	2	AW582792	AW582792 1jk Neuro
c 392	2	20.0	77	2	AW582792	AW582792 1jk Neuro
393	2	20.0	77	3	AY433541	AY433541 Aedes aeg
c 394	2	20.0	77	3	AY433541	AY433541 Aedes aeg
395	2	20.0	77	3	AY440673	AY440673 Armigeres
c 396	2	20.0	77	3	AY440673	AY440673 Armigeres
397	2	20.0	77	4	BG837283	BG837283 Zm10_07g0
c 398	2	20.0	77	4	BG837283	BG837283 Zm10_07g0
399	2	20.0	77	9	CNS00C5Y	AL058467 Drosophil
c 400	2	20.0	77	9	CNS00C5Y	AL058467 Drosophil
401	2	20.0	77	9	CNS00JAE	AL076130 Drosophil
c 402	2	20.0	77	9	CNS00JAE	AL076130 Drosophil
403	2	20.0	77	9	CNS025TN	AL182516 Tetraodon
c 404	2	20.0	77	9	CNS025TN	AL182516 Tetraodon
405	2	20.0	77	9	CNS030XM	AL222835 Tetraodon
c 406	2	20.0	77	9	CNS030XM	AL222835 Tetraodon
407	2	20.0	78	3	AY433574	AY433574 Aedes aeg
c 408	2	20.0	78	3	AY433574	AY433574 Aedes aeg
409	2	20.0	78	3	AY440042	AY440042 Armigeres
c 410	2	20.0	78	3	AY440042	AY440042 Armigeres
411	2	20.0	78	7	CN852403	CN852403 G73 Galle
c 412	2	20.0	78	7	CN852403	CN852403 G73 Galle
413	2	20.0	78	9	CNS00EZR	AL069654 Drosophil
c 414	2	20.0	78	9	CNS00EZR	AL069654 Drosophil
415	2	20.0	78	9	CNS02NPX	AL205710 Tetraodon
c 416	2	20.0	78	9	CNS02NPX	AL205710 Tetraodon
417	2	20.0	78	9	CNS03193	AL223248 Tetraodon
c 418	2	20.0	78	9	CNS03193	AL223248 Tetraodon
419	2	20.0	78	9	CNS03B4L	AL236046 Tetraodon
c 420	2	20.0	78	9	CNS03B4L	AL236046 Tetraodon
421	2	20.0	78	9	CNS03FSU	AL242103 Tetraodon
c 422	2	20.0	78	9	CNS03FSU	AL242103 Tetraodon
423	2	20.0	78	9	CNS03FU4	AL242149 Tetraodon
c 424	2	20.0	78	9	CNS03FU4	AL242149 Tetraodon
425	2	20.0	78	9	CNS044A0	AL273825 Tetraodon
c 426	2	20.0	78	9	CNS044A0	AL273825 Tetraodon
427	2	20.0	78	9	CNS04DFF	AL285684 Tetraodon
c 428	2	20.0	78	9	CNS04DFF	AL285684 Tetraodon
429	2	20.0	79	6	CD457690	CD457690 Fg04d_03a
c 430	2	20.0	79	6	CD457690	CD457690 Fg04d_03a
431	2	20.0	79	9	CNS003KM	AL064929 Drosophil
c 432	2	20.0	79	9	CNS003KM	AL064929 Drosophil
433	2	20.0	79	9	CNS0066J	AL062856 Drosophil
c 434	2	20.0	79	9	CNS0066J	AL062856 Drosophil
435	2	20.0	79	9	CNS00A61	AL054768 Drosophil
c 436	2	20.0	79	9	CNS00A61	AL054768 Drosophil
437	2	20.0	79	9	CNS02F6H	AL194642 Tetraodon
c 438	2	20.0	79	9	CNS02F6H	AL194642 Tetraodon
439	2	20.0	79	9	CNS03O4M	AL252895 Tetraodon
c 440	2	20.0	79	9	CNS03O4M	AL252895 Tetraodon
441	2	20.0	79	9	CNS03P67	AL254248 Tetraodon
c 442	2	20.0	79	9	CNS03P67	AL254248 Tetraodon
443	2	20.0	79	9	CNS03UKX	AL261258 Tetraodon
c 444	2	20.0	79	9	CNS03UKX	AL261258 Tetraodon
445	2	20.0	79	9	CNS045UN	AL275864 Tetraodon
c 446	2	20.0	79	9	CNS045UN	AL275864 Tetraodon
447	2	20.0	79	9	CNS04GVO	AL290157 Tetraodon
c 448	2	20.0	79	9	CNS04GVO	AL290157 Tetraodon
449	2	20.0	80	1	AF211579	AF211579 AF211579
c 450	2	20.0	80	1	AF211579	AF211579 AF211579
451	2	20.0	80	3	AY439823	AY439823 Armigeres
c 452	2	20.0	80	3	AY439823	AY439823 Armigeres
453	2	20.0	80	5	BU238494	BU238494 Ds01_15c0
c 454	2	20.0	80	5	BU238494	BU238494 Ds01_15c0
455	2	20.0	80	7	N55635	N55635 ESTG183 Rat
c 456	2	20.0	80	7	N55635	N55635 ESTG183 Rat
457	2	20.0	80	9	CNS01YGN	AL172976 Tetraodon
c 458	2	20.0	80	9	CNS01YGN	AL172976 Tetraodon
459	2	20.0	80	9	CNS02JQ4	AL200533 Tetraodon
c 460	2	20.0	80	9	CNS02JQ4	AL200533 Tetraodon
461	2	20.0	80	9	CNS02LRO	AL203181 Tetraodon
c 462	2	20.0	80	9	CNS02LRO	AL203181 Tetraodon
463	2	20.0	80	9	CNS03IRP	AL245950 Tetraodon
c 464	2	20.0	80	9	CNS03IRP	AL245950 Tetraodon
465	2	20.0	80	9	CNS03V9F	AL262140 Tetraodon
c 466	2	20.0	80	9	CNS03V9F	AL262140 Tetraodon
467	2	20.0	81	3	AY440495	AY440495 Armigeres
c 468	2	20.0	81	3	AY440495	AY440495 Armigeres
469	2	20.0	81	5	BQ704805	BQ704805 Bn01_01p1
c 470	2	20.0	81	5	BQ704805	BQ704805 Bn01_01p1
471	2	20.0	81	9	CNS01Y8M	AL172687 Tetraodon
c 472	2	20.0	81	9	CNS01Y8M	AL172687 Tetraodon
473	2	20.0	81	9	CNS02KMP	AL201706 Tetraodon
c 474	2	20.0	81	9	CNS02KMP	AL201706 Tetraodon
475	2	20.0	81	9	CNS04K3J	AL294328 Tetraodon
c 476	2	20.0	81	9	CNS04K3J	AL294328 Tetraodon
477	2	20.0	82	3	AY431186	AY431186 Aedes aeg
c 478	2	20.0	82	3	AY431186	AY431186 Aedes aeg
479	2	20.0	82	3	AY439812	AY439812 Armigeres
c 480	2	20.0	82	3	AY439812	AY439812 Armigeres
481	2	20.0	82	7	N84939	N84939 J1640F Huma
c 482	2	20.0	82	7	N84939	N84939 J1640F Huma
483	2	20.0	82	9	CNS016XB	AL107321 Drosophil
c 484	2	20.0	82	9	CNS016XB	AL107321 Drosophil
485	2	20.0	82	9	CNS025I4	AL182101 Tetraodon
c 486	2	20.0	82	9	CNS025I4	AL182101 Tetraodon
487	2	20.0	83	3	AY431468	AY431468 Aedes aeg
c 488	2	20.0	83	3	AY431468	AY431468 Aedes aeg
489	2	20.0	83	3	AY431573	AY431573 Aedes aeg
c 490	2	20.0	83	3	AY431573	AY431573 Aedes aeg
491	2	20.0	83	3	AY433590	AY433590 Aedes aeg
c 492	2	20.0	83	3	AY433590	AY433590 Aedes aeg
493	2	20.0	83	7	T24924	T24924 EST499 Huma
c 494	2	20.0	83	7	T24924	T24924 EST499 Huma
495	2	20.0	83	9	CNS02D56	AL192003 Tetraodon
c 496	2	20.0	83	9	CNS02D56	AL192003 Tetraodon
497	2	20.0	83	9	CNS03BJA	AL236575 Tetraodon
c 498	2	20.0	83	9	CNS03BJA	AL236575 Tetraodon
499	2	20.0	83	9	CNS03XK9	AL265122 Tetraodon
c 500	2	20.0	83	9	CNS03XK9	AL265122 Tetraodon
501	2	20.0	84	3	AY431112	AY431112 Aedes aeg
c 502	2	20.0	84	3	AY431112	AY431112 Aedes aeg
503	2	20.0	84	3	AY431195	AY431195 Aedes aeg
c 504	2	20.0	84	3	AY431195	AY431195 Aedes aeg
505	2	20.0	84	3	AY440433	AY440433 Armigeres
c 506	2	20.0	84	3	AY440433	AY440433 Armigeres
507	2	20.0	84	9	CNS02KB5	AL201290 Tetraodon
c 508	2	20.0	84	9	CNS02KB5	AL201290 Tetraodon
509	2	20.0	84	9	CNS02QJJ	AL209368 Tetraodon
c 510	2	20.0	84	9	CNS02QJJ	AL209368 Tetraodon
511	2	20.0	84	9	CNS03VJT	AL262514 Tetraodon
c 512	2	20.0	84	9	CNS03VJT	AL262514 Tetraodon
513	2	20.0	84	9	CNS03ZI6	AL267639 Tetraodon
c 514	2	20.0	84	9	CNS03ZI6	AL267639 Tetraodon
515	2	20.0	84	9	CNS041NL	AL270426 Tetraodon
c 516	2	20.0	84	9	CNS041NL	AL270426 Tetraodon
517	2	20.0	84	9	CNS04MNO	AL297645 Tetraodon
c 518	2	20.0	84	9	CNS04MNO	AL297645 Tetraodon
519	2	20.0	85	1	AF211809	AF211809 AF211809
c 520	2	20.0	85	1	AF211809	AF211809 AF211809
521	2	20.0	85	3	AY433048	AY433048 Aedes aeg
c 522	2	20.0	85	3	AY433048	AY433048 Aedes aeg
523	2	20.0	85	3	AY440490	AY440490 Armigeres
c 524	2	20.0	85	3	AY440490	AY440490 Armigeres
525	2	20.0	85	9	CNS02EGF	AL193704 Tetraodon
c 526	2	20.0	85	9	CNS02EGF	AL193704 Tetraodon
527	2	20.0	85	9	CNS03A1F	AL234636 Tetraodon
c 528	2	20.0	85	9	CNS03A1F	AL234636 Tetraodon
529	2	20.0	85	9	CNS03NF0	AL251973 Tetraodon
c 530	2	20.0	85	9	CNS03NF0	AL251973 Tetraodon
531	2	20.0	85	9	CNS04MB8	AL297197 Tetraodon
c 532	2	20.0	85	9	CNS04MB8	AL297197 Tetraodon
533	2	20.0	86	3	AY439581	AY439581 Armigeres
c 534	2	20.0	86	3	AY439581	AY439581 Armigeres
535	2	20.0	86	3	AY440481	AY440481 Armigeres

c	536	2	20.0	86	3	AY440481	AY440481	Armigeres		609	2	20.0	89	9	CNS04G2O	AL289113	Tetraodon
	537	2	20.0	86	9	CNS00GY1	AL072689	Drosophil	c	610	2	20.0	89	9	CNS04G2O	AL289113	Tetraodon
c	538	2	20.0	86	9	CNS00GY1	AL072689	Drosophil		611	2	20.0	89	9	CNS04J97	AL293236	Tetraodon
	539	2	20.0	86	9	CNS01SSB	AL165620	Tetraodon	c	612	2	20.0	89	9	CNS04J97	AL293236	Tetraodon
c	540	2	20.0	86	9	CNS01SSB	AL165620	Tetraodon		613	2	20.0	90	2	AW582788	AW582788	2rhC Neur
	541	2	20.0	86	9	CNS021IJ	AL176932	Tetraodon	c	614	2	20.0	90	2	AW582788	AW582788	2rhC Neur
c	542	2	20.0	86	9	CNS021IJ	AL176932	Tetraodon		615	2	20.0	90	9	CNS010K9	AL099075	Drosophil
	543	2	20.0	86	9	CNS02FGJ	AL195004	Tetraodon	c	616	2	20.0	90	9	CNS010K9	AL099075	Drosophil
c	544	2	20.0	86	9	CNS02FGJ	AL195004	Tetraodon		617	2	20.0	90	9	CNS03AOA	AL235459	Tetraodon
	545	2	20.0	86	9	CNS02PYH	AL208610	Tetraodon	c	618	2	20.0	90	9	CNS03AOA	AL235459	Tetraodon
c	546	2	20.0	86	9	CNS02PYH	AL208610	Tetraodon		619	2	20.0	90	9	CNS03X7V	AL264676	Tetraodon
	547	2	20.0	86	9	CNS03NLI	AL252207	Tetraodon	c	620	2	20.0	90	9	CNS03X7V	AL264676	Tetraodon
c	548	2	20.0	86	9	CNS03NLI	AL252207	Tetraodon		621	2	20.0	91	2	AW455211	AW455211	1rk Neuro
	549	2	20.0	86	9	CNS04GPP	AL289942	Tetraodon	c	622	2	20.0	91	2	AW455211	AW455211	1rk Neuro
c	550	2	20.0	86	9	CNS04GPP	AL289942	Tetraodon		623	2	20.0	91	3	AY431378	AY431378	Aedes aeg
	551	2	20.0	86	9	CNS04JXY	AL294127	Tetraodon	c	624	2	20.0	91	3	AY431378	AY431378	Aedes aeg
c	552	2	20.0	86	9	CNS04JXY	AL294127	Tetraodon		625	2	20.0	91	3	AY440500	AY440500	Armigeres
	553	2	20.0	86	9	CNS04LIP	AL296170	Tetraodon	c	626	2	20.0	91	3	AY440500	AY440500	Armigeres
c	554	2	20.0	86	9	CNS04LIP	AL296170	Tetraodon		627	2	20.0	91	7	CN813428	CN813428	Fg06_07a0
	555	2	20.0	87	1	AA231948	AA231948	AS3ISB003	c	628	2	20.0	91	7	CN813428	CN813428	Fg06_07a0
c	556	2	20.0	87	1	AA231948	AA231948	AS3ISB003		629	2	20.0	91	7	L46987	L46987	SCMRAP074 C
	557	2	20.0	87	2	AW444385	AW444385	AB513 Pri	c	630	2	20.0	91	7	L46987	L46987	SCMRAP074 C
c	558	2	20.0	87	2	AW444385	AW444385	AB513 Pri		631	2	20.0	91	9	CNS02TFY	AL213127	Tetraodon
	559	2	20.0	87	3	AY433208	AY433208	Aedes aeg	c	632	2	20.0	91	9	CNS02TFY	AL213127	Tetraodon
c	560	2	20.0	87	3	AY433208	AY433208	Aedes aeg		633	2	20.0	91	9	CNS03BVX	AL237030	Tetraodon
	561	2	20.0	87	3	AY433366	AY433366	Aedes aeg	c	634	2	20.0	91	9	CNS03BVX	AL237030	Tetraodon
c	562	2	20.0	87	3	AY433366	AY433366	Aedes aeg		635	2	20.0	92	1	AJ283197	AJ283197	4A3A-P7H1
	563	2	20.0	87	9	CNS00I1T	AL074323	Drosophil	c	636	2	20.0	92	1	AJ283197	AJ283197	4A3A-P7H1
c	564	2	20.0	87	9	CNS00I1T	AL074323	Drosophil		637	2	20.0	92	2	AW059583	AW059583	HuTH.bsst
	565	2	20.0	87	9	CNS012UH	AL102035	Drosophil	c	638	2	20.0	92	2	AW059583	AW059583	HuTH.bsst
c	566	2	20.0	87	9	CNS012UH	AL102035	Drosophil		639	2	20.0	92	3	AY432337	AY432337	Aedes aeg
	567	2	20.0	87	9	CNS01ZBQ	AL174095	Tetraodon	c	640	2	20.0	92	3	AY432337	AY432337	Aedes aeg
c	568	2	20.0	87	9	CNS01ZBQ	AL174095	Tetraodon		641	2	20.0	92	7	L46963	L46963	SCMRAP050 C
	569	2	20.0	87	9	CNS0238Y	AL179179	Tetraodon	c	642	2	20.0	92	7	L46963	L46963	SCMRAP050 C
c	570	2	20.0	87	9	CNS0238Y	AL179179	Tetraodon		643	2	20.0	92	7	T25154	T25154	EST729 Huma
	571	2	20.0	87	9	CNS02VPL	AL216066	Tetraodon	c	644	2	20.0	92	7	T25154	T25154	EST729 Huma
c	572	2	20.0	87	9	CNS02VPL	AL216066	Tetraodon		645	2	20.0	92	9	CNS005AX	AL057857	Drosophil
	573	2	20.0	87	9	CNS03KZC	AL248817	Tetraodon	c	646	2	20.0	92	9	CNS005AX	AL057857	Drosophil
c	574	2	20.0	87	9	CNS03KZC	AL248817	Tetraodon		647	2	20.0	92	9	CNS011DU	AL100140	Drosophil
	575	2	20.0	87	9	CNS04AS9	AL282258	Tetraodon	c	648	2	20.0	92	9	CNS011DU	AL100140	Drosophil
c	576	2	20.0	87	9	CNS04AS9	AL282258	Tetraodon		649	2	20.0	93	1	AF211665	AF211665	
	577	2	20.0	87	9	CNS04P1X	AL300750	Tetraodon	c	650	2	20.0	93	1	AF211665	AF211665	
c	578	2	20.0	87	9	CNS04P1X	AL300750	Tetraodon		651	2	20.0	93	2	BE217190	BE217190	2008AEDM
	579	2	20.0	87	9	CNS04PIJ	AL301348	Tetraodon	c	652	2	20.0	93	2	BE217190	BE217190	2008AEDM
c	580	2	20.0	87	9	CNS04PIJ	AL301348	Tetraodon		653	2	20.0	93	3	AY439491	AY439491	Armigeres
	581	2	20.0	88	2	AW444353	AW444353	AB428 Pri	c	654	2	20.0	93	3	AY439491	AY439491	Armigeres
c	582	2	20.0	88	2	AW444353	AW444353	AB428 Pri		655	2	20.0	93	3	AY440370	AY440370	Armigeres
	583	2	20.0	88	3	AY440693	AY440693	Armigeres	c	656	2	20.0	93	3	AY440370	AY440370	Armigeres
c	584	2	20.0	88	3	AY440693	AY440693	Armigeres		657	2	20.0	93	3	AY441413	AY441413	Armigeres
	585	2	20.0	88	9	CNS0046A	AL066315	Drosophil	c	658	2	20.0	93	3	AY441413	AY441413	Armigeres
c	586	2	20.0	88	9	CNS0046A	AL066315	Drosophil		659	2	20.0	93	9	CNS00795	AL066670	Drosophil
	587	2	20.0	88	9	CNS02FXH	AL195614	Tetraodon	c	660	2	20.0	93	9	CNS00795	AL066670	Drosophil
c	588	2	20.0	88	9	CNS02FXH	AL195614	Tetraodon		661	2	20.0	93	9	CNS00ZCN	AL097505	Drosophil
	589	2	20.0	88	9	CNS02GFS	AL196273	Tetraodon	c	662	2	20.0	93	9	CNS00ZCN	AL097505	Drosophil
c	590	2	20.0	88	9	CNS02GFS	AL196273	Tetraodon		663	2	20.0	93	9	CNS0171O	AL107478	Drosophil
	591	2	20.0	89	3	AY440689	AY440689	Armigeres	c	664	2	20.0	93	9	CNS0171O	AL107478	Drosophil
c	592	2	20.0	89	3	AY440689	AY440689	Armigeres		665	2	20.0	93	9	CNS01T1X	AL165966	Tetraodon
	593	2	20.0	89	6	CB686411	CB686411	Bn01b_04h	c	666	2	20.0	93	9	CNS01T1X	AL165966	Tetraodon
c	594	2	20.0	89	6	CB686411	CB686411	Bn01b_04h		667	2	20.0	93	9	CNS029BF	AL187044	Tetraodon
	595	2	20.0	89	8	AF219015	AF219015	AF219015	c	668	2	20.0	93	9	CNS029BF	AL187044	Tetraodon
c	596	2	20.0	89	8	AF219015	AF219015	AF219015		669	2	20.0	93	9	CNS03FHU	AL241707	Tetraodon
	597	2	20.0	89	9	CNS00JC6	AL075992	Drosophil	c	670	2	20.0	93	9	CNS03FHU	AL241707	Tetraodon
c	598	2	20.0	89	9	CNS00JC6	AL075992	Drosophil		671	2	20.0	93	9	CNS03IFL	AL245514	Tetraodon
	599	2	20.0	89	9	CNS01YJC	AL173073	Tetraodon	c	672	2	20.0	93	9	CNS03IFL	AL245514	Tetraodon
c	600	2	20.0	89	9	CNS01YJC	AL173073	Tetraodon		673	2	20.0	93	9	CNS03WWC	AL264261	Tetraodon
	601	2	20.0	89	9	CNS025K1	AL182170	Tetraodon	c	674	2	20.0	93	9	CNS03WWC	AL264261	Tetraodon
c	602	2	20.0	89	9	CNS025K1	AL182170	Tetraodon		675	2	20.0	94	2	AW444177	AW444177	AB320 Bas
	603	2	20.0	89	9	CNS02NCV	AL205240	Tetraodon	c	676	2	20.0	94	2	AW444177	AW444177	AB320 Bas
c	604	2	20.0	89	9	CNS02NCV	AL205240	Tetraodon		677	2	20.0	94	6	CD457338	CD457338	Fg05_02m1
	605	2	20.0	89	9	CNS02QOZ	AL209564	Tetraodon	c	678	2	20.0	94	6	CD457338	CD457338	Fg05_02m1
c	606	2	20.0	89	9	CNS02QOZ	AL209564	Tetraodon		679	2	20.0	94	9	CNS008IY	AL052136	Drosophil
	607	2	20.0	89	9	CNS03DTD	AL239530	Tetraodon	c	680	2	20.0	94	9	CNS008IY	AL052136	Drosophil
c	608	2	20.0	89	9	CNS03DTD	AL239530	Tetraodon		681	2	20.0	94	9	CNS011G8	AL100226	Drosophil

c 682	2	20.0	94	9	CNS011G8	AL100226	Drosophil
683	2	20.0	94	9	CNS0170X	AL107451	Drosophil
c 684	2	20.0	94	9	CNS0170X	AL107451	Drosophil
685	2	20.0	94	9	CNS02QIM	AL209335	Tetraodon
c 686	2	20.0	94	9	CNS02QIM	AL209335	Tetraodon
687	2	20.0	95	1	AI001441	AI001441	EST0022 T
c 688	2	20.0	95	1	AI001441	AI001441	EST0022 T
689	2	20.0	95	2	AW497636	AW497636	RPS20G5B8
c 690	2	20.0	95	2	AW497636	AW497636	RPS20G5B8
691	2	20.0	95	2	AW621134	AW621134	2ji Neuro
c 692	2	20.0	95	2	AW621134	AW621134	2ji Neuro
693	2	20.0	95	3	AY440569	AY440569	Armigeres
c 694	2	20.0	95	3	AY440569	AY440569	Armigeres
695	2	20.0	95	6	CD649674	CD649674	CvGil0037
c 696	2	20.0	95	6	CD649674	CD649674	CvGil0037
697	2	20.0	95	9	CNS025GK	AL182045	Tetraodon
c 698	2	20.0	95	9	CNS025GK	AL182045	Tetraodon
699	2	20.0	95	9	CNS02OR2	AL207047	Tetraodon
c 700	2	20.0	95	9	CNS02OR2	AL207047	Tetraodon
701	2	20.0	95	9	CNS02RN5	AL210794	Tetraodon
c 702	2	20.0	95	9	CNS02RN5	AL210794	Tetraodon
703	2	20.0	95	9	CNS03WCO	AL263553	Tetraodon
c 704	2	20.0	95	9	CNS03WCO	AL263553	Tetraodon
705	2	20.0	96	3	AY432683	AY432683	Aedes aeg
c 706	2	20.0	96	3	AY432683	AY432683	Aedes aeg
707	2	20.0	96	3	AY439832	AY439832	Armigeres
c 708	2	20.0	96	3	AY439832	AY439832	Armigeres
709	2	20.0	96	3	AY440135	AY440135	Armigeres
c 710	2	20.0	96	3	AY440135	AY440135	Armigeres
711	2	20.0	96	7	L76125	L76125	SCMRAP0219
c 712	2	20.0	96	7	L76125	L76125	SCMRAP0219
713	2	20.0	96	9	CNS01136	AL099756	Drosophil
c 714	2	20.0	96	9	CNS01136	AL099756	Drosophil
715	2	20.0	96	9	CNS011N0	AL100470	Drosophil
c 716	2	20.0	96	9	CNS011N0	AL100470	Drosophil
717	2	20.0	96	9	CNS02R1G	AL210013	Tetraodon
c 718	2	20.0	96	9	CNS02R1G	AL210013	Tetraodon
719	2	20.0	97	1	AF211555	AF211555	AF211555
c 720	2	20.0	97	1	AF211555	AF211555	AF211555
721	2	20.0	97	1	AJ282937	AJ282937	4A3A-P2A1
c 722	2	20.0	97	1	AJ282937	AJ282937	4A3A-P2A1
723	2	20.0	97	2	AW059611	AW059611	HuTH.bsst
c 724	2	20.0	97	2	AW059611	AW059611	HuTH.bsst
725	2	20.0	97	3	AY439456	AY439456	Armigeres
c 726	2	20.0	97	3	AY439456	AY439456	Armigeres
727	2	20.0	97	9	CNS010GZ	AL098957	Drosophil
c 728	2	20.0	97	9	CNS010GZ	AL098957	Drosophil
729	2	20.0	97	9	CNS01YLD	AL173146	Tetraodon
c 730	2	20.0	97	9	CNS01YLD	AL173146	Tetraodon
731	2	20.0	97	9	CNS02DFI	AL192375	Tetraodon
c 732	2	20.0	97	9	CNS02DFI	AL192375	Tetraodon
733	2	20.0	97	9	CNS02VXN	AL216356	Tetraodon
c 734	2	20.0	97	9	CNS02VXN	AL216356	Tetraodon
735	2	20.0	97	9	CNS03B08	AL235889	Tetraodon
c 736	2	20.0	97	9	CNS03B08	AL235889	Tetraodon
737	2	20.0	97	9	CNS03BEK	AL236405	Tetraodon
c 738	2	20.0	97	9	CNS03BEK	AL236405	Tetraodon
739	2	20.0	97	9	CNS03D3H	AL238598	Tetraodon
c 740	2	20.0	97	9	CNS03D3H	AL238598	Tetraodon
741	2	20.0	98	2	AW466364	AW466364	gh59a7b27
c 742	2	20.0	98	2	AW466364	AW466364	gh59a7b27
743	2	20.0	98	3	AY431591	AY431591	Aedes aeg
c 744	2	20.0	98	3	AY431591	AY431591	Aedes aeg
745	2	20.0	98	3	AY433487	AY433487	Aedes aeg
c 746	2	20.0	98	3	AY433487	AY433487	Aedes aeg
747	2	20.0	98	7	CN811517	CN811517	Fg13_01m2
c 748	2	20.0	98	7	CN811517	CN811517	Fg13_01m2
749	2	20.0	98	9	CNS00CKL	AL059196	Drosophil
c 750	2	20.0	98	9	CNS00CKL	AL059196	Drosophil
751	2	20.0	98	9	CNS00I3F	AL074381	Drosophil
c 752	2	20.0	98	9	CNS00I3F	AL074381	Drosophil
753	2	20.0	98	9	CNS04PYV	AL301936	Tetraodon
c 754	2	20.0	98	9	CNS04PYV	AL301936	Tetraodon
755	2	20.0	99	3	AY431446	AY431446	Aedes aeg
c 756	2	20.0	99	3	AY431446	AY431446	Aedes aeg
757	2	20.0	99	3	AY431503	AY431503	Aedes aeg
c 758	2	20.0	99	3	AY431503	AY431503	Aedes aeg
759	2	20.0	99	3	AY432126	AY432126	Aedes aeg
c 760	2	20.0	99	3	AY432126	AY432126	Aedes aeg
761	2	20.0	99	9	CNS004DR	AL051310	Drosophil
c 762	2	20.0	99	9	CNS004DR	AL051310	Drosophil
763	2	20.0	99	9	CNS027LM	AL184819	Tetraodon
c 764	2	20.0	99	9	CNS027LM	AL184819	Tetraodon
765	2	20.0	99	9	CNS036R8	AL230381	Tetraodon
c 766	2	20.0	99	9	CNS036R8	AL230381	Tetraodon
767	2	20.0	99	9	CNS03AEJ	AL235108	Tetraodon
c 768	2	20.0	99	9	CNS03AEJ	AL235108	Tetraodon
769	2	20.0	99	9	CNS06ULL	AL415999	T7 end of
c 770	2	20.0	99	9	CNS06ULL	AL415999	T7 end of
771	2	20.0	100	1	AI617502	AI617502	zehn1689.
c 772	2	20.0	100	1	AI617502	AI617502	zehn1689.
773	2	20.0	100	2	AW621120	AW621120	ERaD3g24_
c 774	2	20.0	100	2	AW621120	AW621120	ERaD3g24_
775	2	20.0	100	3	AY431923	AY431923	Aedes aeg
c 776	2	20.0	100	3	AY431923	AY431923	Aedes aeg
777	2	20.0	100	3	AY432099	AY432099	Aedes aeg
c 778	2	20.0	100	3	AY432099	AY432099	Aedes aeg
779	2	20.0	100	3	AY440198	AY440198	Armigeres
c 780	2	20.0	100	3	AY440198	AY440198	Armigeres
781	2	20.0	100	5	BQ640980	BQ640980	SSH-Bbblc
c 782	2	20.0	100	5	BQ640980	BQ640980	SSH-Bbblc
783	2	20.0	100	9	CNS00CGH	AL059250	Drosophil
c 784	2	20.0	100	9	CNS00CGH	AL059250	Drosophil
785	2	20.0	100	9	CNS03SM2	AL258707	Tetraodon
c 786	2	20.0	100	9	CNS03SM2	AL258707	Tetraodon
787	2	20.0	100	9	CNS06UXS	AL416438	T7 end of
c 788	2	20.0	100	9	CNS06UXS	AL416438	T7 end of
789	1	10.0	2	1	AL039341	AL039341	DKFZp434F
c 790	1	10.0	2	1	AL039341	AL039341	DKFZp434F
791	1	10.0	2	1	AL042337	AL042337	DKFZp434O
c 792	1	10.0	2	1	AL042337	AL042337	DKFZp434O
793	1	10.0	2	1	AL043859	AL043859	DKFZp434B
c 794	1	10.0	2	1	AL043859	AL043859	DKFZp434B
795	1	10.0	2	1	AL047069	AL047069	DKFZp586P
c 796	1	10.0	2	1	AL047069	AL047069	DKFZp586P
797	1	10.0	2	5	BX266185	BX266185	BX266185
c 798	1	10.0	2	5	BX266185	BX266185	BX266185
799	1	10.0	2	5	BX266563	BX266563	BX266563
c 800	1	10.0	2	5	BX266563	BX266563	BX266563
801	1	10.0	2	5	BX267110	BX267110	BX267110
c 802	1	10.0	2	5	BX267110	BX267110	BX267110
803	1	10.0	2	5	BX267118	BX267118	BX267118
c 804	1	10.0	2	5	BX267118	BX267118	BX267118
805	1	10.0	2	6	CA850819	CA850819	D06H04_H0
c 806	1	10.0	2	6	CA850819	CA850819	D06H04_H0
807	1	10.0	2	6	CA850842	CA850842	D07B06_C1
c 808	1	10.0	2	6	CA850842	CA850842	D07B06_C1
809	1	10.0	2	6	CA851273	CA851273	D12A01_B1
c 810	1	10.0	2	6	CA851273	CA851273	D12A01_B1
811	1	10.0	2	6	CF280384	CF280384	14ETL--07
c 812	1	10.0	2	6	CF280384	CF280384	14ETL--07
813	1	10.0	2	6	CF280511	CF280511	14ETL--07
c 814	1	10.0	2	6	CF280511	CF280511	14ETL--07
815	1	10.0	2	6	CF281609	CF281609	14ETL--08
c 816	1	10.0	2	6	CF281609	CF281609	14ETL--08
817	1	10.0	2	6	CF291112	CF291112	14ROOT--0
c 818	1	10.0	2	6	CF291112	CF291112	14ROOT--0
819	1	10.0	2	6	CF299550	CF299550	7LEAF--03
c 820	1	10.0	2	6	CF299550	CF299550	7LEAF--03
821	1	10.0	2	6	CF299820	CF299820	7LEAF--03
c 822	1	10.0	2	6	CF299820	CF299820	7LEAF--03
823	1	10.0	2	6	CF301411	CF301411	7LEAF--06
c 824	1	10.0	2	6	CF301411	CF301411	7LEAF--06
825	1	10.0	2	6	CF306288	CF306288	HDA1--03-
c 826	1	10.0	2	6	CF306288	CF306288	HDA1--03-
827	1	10.0	2	6	CF307078	CF307078	HDA1--05-

c 828	1	10.0	2	6	CF307078	CF307078 HDA1--05-
829	1	10.0	2	6	CF307123	CF307123 HDA1--05-
c 830	1	10.0	2	6	CF307123	CF307123 HDA1--05-
831	1	10.0	2	6	CF307878	CF307878 ABF--01-H
c 832	1	10.0	2	6	CF307878	CF307878 ABF--01-H
833	1	10.0	2	6	CF311389	CF311389 ABF--06-J
c 834	1	10.0	2	6	CF311389	CF311389 ABF--06-J
835	1	10.0	2	6	CF311851	CF311851 ABF--07-E
c 836	1	10.0	2	6	CF311851	CF311851 ABF--07-E
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867	1	10.0	2	9	CL673395	CL673395 PRI019b_G
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869	1	10.0	2	9	CL677053	CL677053 PRI011b_B
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c 884	1	10.0	2	9	CL688890	CL688890 PRI014d_A
885	1	10.0	2	9	CL688912	CL688912 PRI014d_C
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c 896	1	10.0	3	5	BX267257	BX267257 BX267257
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c 898	1	10.0	3	6	CA850938	CA850938 D08D06_H1
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c 900	1	10.0	3	6	CA851600	CA851600 D15E06_I1
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c 902	1	10.0	3	6	CA851961	CA851961 D19E06_I1
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c 908	1	10.0	3	6	CF296126	CF296126 30DGS--06
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929	1	10.0	3	6	CF306855	CF306855 HDA1--05-
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c 936	1	10.0	3	6	CF306992	CF306992 HDA1--05-
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947	1	10.0	3	6	CF307117	CF307117 HDA1--05-
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c 966	1	10.0	3	6	CF307489	CF307489 HDA1--06-
967	1	10.0	3	6	CF307511	CF307511 HDA1--06-
c 968	1	10.0	3	6	CF307511	CF307511 HDA1--06-
969	1	10.0	3	6	CF307516	CF307516 HDA1--06-
c 970	1	10.0	3	6	CF307516	CF307516 HDA1--06-
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975	1	10.0	3	6	CF309377	CF309377 ABF--03-I
c 976	1	10.0	3	6	CF309377	CF309377 ABF--03-I
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c 978	1	10.0	3	6	CF310006	CF310006 ABF--04-H
979	1	10.0	3	6	CF311041	CF311041 ABF--06-B
c 980	1	10.0	3	6	CF311041	CF311041 ABF--06-B
981	1	10.0	3	6	CF311214	CF311214 ABF--06-F
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983	1	10.0	3	6	CF311628	CF311628 ABF--06-O
c 984	1	10.0	3	6	CF311628	CF311628 ABF--06-O
985	1	10.0	3	6	CF313258	CF313258 HD--01-F0
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989	1	10.0	3	6	CF315183	CF315183 HD--04-A0
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991	1	10.0	3	6	CF315632	CF315632 HD--04-K0
c 992	1	10.0	3	6	CF315632	CF315632 HD--04-K0
993	1	10.0	3	6	CF317717	CF317717 HD--07-I0
c 994	1	10.0	3	6	CF317717	CF317717 HD--07-I0
995	1	10.0	3	6	CF322001	CF322001 HD--13-H0
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997	1	10.0	3	6	CF327094	CF327094 NACL--01-
c 998	1	10.0	3	6	CF327094	CF327094 NACL--01-
999	1	10.0	3	6	CF334168	CF334168 JMT--03-F
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ALIGNMENTS

RESULT 1
CNS015BQ
LOCUS CNS015BQ 74 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACN13P24 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL105248
VERSION AL105248.1 GI:5617262
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 74)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .74
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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/clone="BACN13P24"
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/note="end : SP6"
ORIGIN

Query Match 40.0%; Score 4; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWWG 7
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Db 68 CWWG 71

RESULT 2
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LOCUS CNS015BQ 74 bp DNA linear GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC BACN13P24 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL105248
VERSION AL105248.1 GI:5617262
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 74)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
FEATURES Location/Qualifiers
source 1. .74
/organism="Drosophila melanogaster"
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/clone="BACN13P24"
/clone_lib="DrosBAC"
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Query Match 40.0%; Score 4; DB 9; Length 74;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWWG 7
||||
Db 71 CWWG 68

RESULT 3
AF211608
LOCUS AF211608 77 bp mRNA linear EST 31-DEC-2000
DEFINITION AF211608 34.1B Nicotiana tabacum cDNA clone fragment 79, mRNA sequence.
ACCESSION AF211608
VERSION AF211608.1 GI:11999989
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 77)
AUTHORS Durrant,W.E., Rowland,O., Piedras,P., Hammond-Kosack,K.E. and Jones,J.D.G.
TITLE cDNA expression profiling reveals rapid, resistance gene-dependent, active oxygen-independent, gene induction during the plant defence

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            response
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Durrant WE
            Sainsbury Laboratory
            John Innes Centre
            Colney Lane, Norwich, Norfolk NR4 7UH, UK
            Email: wendy.durrant@bbsrc.ac.uk
            rapidly induced, oxidative burst independent cDNA-AFLP fragment.
FEATURES             Location/Qualifiers
     source          1. .77
                     /organism="Nicotiana tabacum"
                     /mol_type="mRNA"
                     /cultivar="Petite Havana"
                     /db_xref="taxon:4097"
                     /clone="fragment 79"
                     /clone_lib="34.1B"
                     /note="cell suspension cultures harvested 30 min after
                     treatment with the Avr9 peptide from the fungus
                     Cladosporium fulvum; 34.1B tobacco contains Cf-9
                     resistance gene"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 1;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRCW 5
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Db         30 RRCW 33


RESULT 4
AF211608/c
LOCUS       AF211608                  77 bp    mRNA    linear   EST 31-DEC-2000
DEFINITION  AF211608 34.1B Nicotiana tabacum cDNA clone fragment 79, mRNA
            sequence.
ACCESSION   AF211608
VERSION     AF211608.1  GI:11999989
KEYWORDS    EST.
SOURCE      Nicotiana tabacum (common tobacco)
  ORGANISM  Nicotiana tabacum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1  (bases 1 to 77)
  AUTHORS   Durrant,W.E., Rowland,O., Piedras,P., Hammond-Kosack,K.E. and
            Jones,J.D.G.
  TITLE     cDNA expression profiling reveals rapid, resistance gene-dependent,
            active oxygen-independent, gene induction during the plant defence
            response
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Durrant WE
            Sainsbury Laboratory
            John Innes Centre
            Colney Lane, Norwich, Norfolk NR4 7UH, UK
            Email: wendy.durrant@bbsrc.ac.uk
            rapidly induced, oxidative burst independent cDNA-AFLP fragment.
FEATURES             Location/Qualifiers
     source          1. .77
                     /organism="Nicotiana tabacum"
                     /mol_type="mRNA"
                     /cultivar="Petite Havana"
                     /db_xref="taxon:4097"
                     /clone="fragment 79"
                     /clone_lib="34.1B"
                     /note="cell suspension cultures harvested 30 min after
                     treatment with the Avr9 peptide from the fungus
                     Cladosporium fulvum; 34.1B tobacco contains Cf-9
                     resistance gene"
ORIGIN

  Query Match             40.0%;  Score 4;  DB 1;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WGYY 9
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Db         33 WGYY 30


RESULT 5
AY431131
LOCUS       AY431131                  63 bp    mRNA    linear   HTC 23-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 38277 unknown mRNA sequence.
ACCESSION   AY431131
VERSION     AY431131.1  GI:42762112
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 63)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
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                     /db_xref="taxon:7159"
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                     /note="ASAP-UW Feature ID: 38276"
     misc_feature    1. .63
                     /note="unknown; ASAP-UW Feature ID: 38277"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 3;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RCW 5
              |||
Db         30 RCW 32


RESULT 6
AY431131/c
LOCUS       AY431131                  63 bp    mRNA    linear   HTC 23-JUN-2004
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DEFINITION  Aedes aegypti ASAP ID: 38277 unknown mRNA sequence.
ACCESSION   AY431131
VERSION     AY431131.1  GI:42762112
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 63)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 63)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .63
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 38276"
     misc_feature    1. .63
                     /note="unknown; ASAP-UW Feature ID: 38277"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 3;  Length 63;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WGY 8
              |||
Db         32 WGY 30


RESULT 7
CNS011MQ
LOCUS       CNS011MQ                  68 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN06B15 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL100460
VERSION     AL100460.1  GI:5612071
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 68)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .68
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN06B15"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 9;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          1 CWW 3


RESULT 8
CNS011MQ/c
LOCUS       CNS011MQ                  68 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN06B15 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL100460
VERSION     AL100460.1  GI:5612071
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 68)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .68
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN06B15"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN
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  Query Match             30.0%;  Score 3;  DB 9;  Length 68;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          3 WWG 1


RESULT 9
T24836
LOCUS       T24836                    70 bp    mRNA    linear   EST 24-AUG-1995
DEFINITION  EST411 Human colorectal cancer Homo sapiens cDNA clone 15C4, mRNA
            sequence.
ACCESSION   T24836
VERSION     T24836.1  GI:534461
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Frigerio,J.-M., Berthezene,P., Garrido,P., Ortiz,E., Barthellemy,S,
            Vasseur,S., Sastre,B., Seleznieff,I., Dagorn,J.-C. and
            Iovanna,J.-L.
  TITLE     Analysis of 2166 clones from a human colorectal cancer cDNA library
            by partial sequencing
  JOURNAL   Hum. Mol. Genet. 4, 37-43 (1995)
  MEDLINE   95227175
   PUBMED   7711732
COMMENT     Contact: Iovanna JL
            U.315 INSERM
            46 Bd de la Gaye, F-13009 Marseille, France.
            Tel: (33) 91 82 03 15
            Fax: (33) 91 26 62 19
            Email: dagorn@arthur.citi2.fr
            This sequence is one of a series obtained by systematic  sequencing
            of a colorectal cancer cDNA library.
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="15C4"
                     /lab_host="E. coli NM522"
                     /clone_lib="Human colorectal cancer"
                     /note="Vector: pT7T3D; Site_1: Eco RI; Site_2: Not I; mRNA
                     was purified from a colorectal tumour of an adult male.
                     cDNA was constructed and cloned into the pT7T3D phagemid
                     following the manufacturer intructions (Pharmacia)."
ORIGIN

  Query Match             30.0%;  Score 3;  DB 7;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db         17 CWW 19


RESULT 10
T24836/c
LOCUS       T24836                    70 bp    mRNA    linear   EST 24-AUG-1995
DEFINITION  EST411 Human colorectal cancer Homo sapiens cDNA clone 15C4, mRNA
            sequence.
ACCESSION   T24836
VERSION     T24836.1  GI:534461
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 70)
  AUTHORS   Frigerio,J.-M., Berthezene,P., Garrido,P., Ortiz,E., Barthellemy,S,
            Vasseur,S., Sastre,B., Seleznieff,I., Dagorn,J.-C. and
            Iovanna,J.-L.
  TITLE     Analysis of 2166 clones from a human colorectal cancer cDNA library
            by partial sequencing
  JOURNAL   Hum. Mol. Genet. 4, 37-43 (1995)
  MEDLINE   95227175
   PUBMED   7711732
COMMENT     Contact: Iovanna JL
            U.315 INSERM
            46 Bd de la Gaye, F-13009 Marseille, France.
            Tel: (33) 91 82 03 15
            Fax: (33) 91 26 62 19
            Email: dagorn@arthur.citi2.fr
            This sequence is one of a series obtained by systematic  sequencing
            of a colorectal cancer cDNA library.
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .70
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="15C4"
                     /lab_host="E. coli NM522"
                     /clone_lib="Human colorectal cancer"
                     /note="Vector: pT7T3D; Site_1: Eco RI; Site_2: Not I; mRNA
                     was purified from a colorectal tumour of an adult male.
                     cDNA was constructed and cloned into the pT7T3D phagemid
                     following the manufacturer intructions (Pharmacia)."
ORIGIN

  Query Match             30.0%;  Score 3;  DB 7;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db         19 WWG 17


RESULT 11
AJ283222
LOCUS       AJ283222                  88 bp    mRNA    linear   EST 30-JUN-2000
DEFINITION  4A3A-P8D3-R Anopheles gambiae immune competent 4A3A Anopheles
            gambiae cDNA clone 4A3A-P8D3, mRNA sequence.
ACCESSION   AJ283222
VERSION     AJ283222.1  GI:6931101
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 88)
  AUTHORS   Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
            Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
            and Kafatos,F.C.
  TITLE     Anopheles gambiae pilot gene discovery project: identification of
            mosquito innate immunity genes from expressed sequence tags
            generated from immune-competent cell lines
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
  MEDLINE   20300950
   PUBMED   10841561
COMMENT     Contact: Dimopoulos G
            Fotis C. Kafatos laboratory
            European Molecular Biology Laboratory
            Meyerhofstrasse 1, 69117 Heidelberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .88
                     /organism="Anopheles gambiae"
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```
                     /mol_type="mRNA"
                     /strain="4A r/r"
                     /db_xref="taxon:7165"
                     /clone="4A3A-P8D3"
                     /cell_line="immune competent 4A3A"
                     /lab_host="E. coli DH10B"
                     /clone_lib="Anopheles gambiae immune competent 4A3A"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from
                     forward priming site which reads from the 3' end of the
                     cDNA. The 4A3A is a directionally cloned and normalized
                     cDNA library that was constructed from the 4A3A cell line
                     oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
                     (1996) : Normalization and Subtraction: Two approaches To
                     Facilitate Gene Discovery, Genome Research 6, 791-806."
ORIGIN

  Query Match             30.0%;  Score 3;  DB 1;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db         39 WWG 41


RESULT 12
AJ283222/c
LOCUS       AJ283222                  88 bp    mRNA    linear   EST 30-JUN-2000
DEFINITION  4A3A-P8D3-R Anopheles gambiae immune competent 4A3A Anopheles
            gambiae cDNA clone 4A3A-P8D3, mRNA sequence.
ACCESSION   AJ283222
VERSION     AJ283222.1  GI:6931101
KEYWORDS    EST.
SOURCE      Anopheles gambiae (African malaria mosquito)
  ORGANISM  Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1  (bases 1 to 88)
  AUTHORS   Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,
            Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
            and Kafatos,F.C.
  TITLE     Anopheles gambiae pilot gene discovery project: identification of
            mosquito innate immunity genes from expressed sequence tags
            generated from immune-competent cell lines
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
  MEDLINE   20300950
   PUBMED   10841561
COMMENT     Contact: Dimopoulos G
            Fotis C. Kafatos laboratory
            European Molecular Biology Laboratory
            Meyerhofstrasse 1, 69117 Heidelberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .88
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /strain="4A r/r"
                     /db_xref="taxon:7165"
                     /clone="4A3A-P8D3"
                     /cell_line="immune competent 4A3A"
                     /lab_host="E. coli DH10B"
                     /clone_lib="Anopheles gambiae immune competent 4A3A"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from
                     forward priming site which reads from the 3' end of the
                     cDNA. The 4A3A is a directionally cloned and normalized
                     cDNA library that was constructed from the 4A3A cell line
                     oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
                     (1996) : Normalization and Subtraction: Two approaches To
                     Facilitate Gene Discovery, Genome Research 6, 791-806."
ORIGIN

  Query Match             30.0%;  Score 3;  DB 1;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db         41 CWW 39


RESULT 13
T24971
LOCUS       T24971                    90 bp    mRNA    linear   EST 24-AUG-1995
DEFINITION  EST546 Human colorectal cancer Homo sapiens cDNA clone 19E1, mRNA
            sequence.
ACCESSION   T24971
VERSION     T24971.1  GI:534596
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Frigerio,J.-M., Berthezene,P., Garrido,P., Ortiz,E., Barthellemy,S,
            Vasseur,S., Sastre,B., Seleznieff,I., Dagorn,J.-C. and
            Iovanna,J.-L.
  TITLE     Analysis of 2166 clones from a human colorectal cancer cDNA library
            by partial sequencing
  JOURNAL   Hum. Mol. Genet. 4, 37-43 (1995)
  MEDLINE   95227175
   PUBMED   7711732
COMMENT     Contact: Iovanna JL
            U.315 INSERM
            46 Bd de la Gaye, F-13009 Marseille, France.
            Tel: (33) 91 82 03 15
            Fax: (33) 91 26 62 19
            Email: dagorn@arthur.citi2.fr
            This sequence is one of a series obtained by systematic  sequencing
            of a colorectal cancer cDNA library.
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .90
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="19E1"
                     /lab_host="E. coli NM522"
                     /clone_lib="Human colorectal cancer"
                     /note="Vector: pT7T3D; Site_1: Eco RI; Site_2: Not I; mRNA
                     was purified from a colorectal tumour of an adult male.
                     cDNA was constructed and cloned into the pT7T3D phagemid
                     following the manufacturer intructions (Pharmacia)."
ORIGIN

  Query Match             30.0%;  Score 3;  DB 7;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db         27 RRC 29


RESULT 14
T24971/c
LOCUS       T24971                    90 bp    mRNA    linear   EST 24-AUG-1995
DEFINITION  EST546 Human colorectal cancer Homo sapiens cDNA clone 19E1, mRNA
            sequence.
ACCESSION   T24971
VERSION     T24971.1  GI:534596
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Frigerio,J.-M., Berthezene,P., Garrido,P., Ortiz,E., Barthellemy,S,
            Vasseur,S., Sastre,B., Seleznieff,I., Dagorn,J.-C. and
            Iovanna,J.-L.
  TITLE     Analysis of 2166 clones from a human colorectal cancer cDNA library
            by partial sequencing
  JOURNAL   Hum. Mol. Genet. 4, 37-43 (1995)
  MEDLINE   95227175
   PUBMED   7711732
COMMENT     Contact: Iovanna JL
            U.315 INSERM
            46 Bd de la Gaye, F-13009 Marseille, France.
            Tel: (33) 91 82 03 15
            Fax: (33) 91 26 62 19
            Email: dagorn@arthur.citi2.fr
            This sequence is one of a series obtained by systematic  sequencing
            of a colorectal cancer cDNA library.
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .90
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="19E1"
                     /lab_host="E. coli NM522"
                     /clone_lib="Human colorectal cancer"
                     /note="Vector: pT7T3D; Site_1: Eco RI; Site_2: Not I; mRNA
                     was purified from a colorectal tumour of an adult male.
                     cDNA was constructed and cloned into the pT7T3D phagemid
                     following the manufacturer intructions (Pharmacia)."
ORIGIN

  Query Match             30.0%;  Score 3;  DB 7;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYY 9
              |||
Db         29 GYY 27


RESULT 15
BQ704626
LOCUS       BQ704626                  91 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  Bn01_03123_A
            Bn01_AAFC_ECORC_transgenic_Brassica_napus_overexpressing_BNCBF17_co
            nstitutively_frost_tolerant Brassica napus cDNA clone Bn01_03123,
            mRNA sequence.
ACCESSION   BQ704626
VERSION     BQ704626.1  GI:21844045
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 91)
  AUTHORS   Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A.,
            Chagnon,J., Farah,S., Couroux,P. and Hattori,J.
  TITLE     Expressed Sequence Tags from constitutively frost tolerant
            transgenic Brassica napus overexpressing BNCBF17
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@agr.gc.ca.
FEATURES             Location/Qualifiers
     source          1. .91
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Westar"
                     /db_xref="taxon:3708"
                     /clone="Bn01_03123"
                     /tissue_type="fourth leaf"
                     /dev_stage="3 weeks seedling grown at room temperature"
                     /clone_lib="Bn01_AAFC_ECORC_transgenic_Brassica_napus_over
                     expressing_BNCBF17_constitutively_frost_tolerant"
                     /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
                     Site_2: XhoI; Germinated in soil flats and seedlings grown
                     for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr
                     light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves
                     collected at 9 am and immediately frozen."
ORIGIN

  Query Match             30.0%;  Score 3;  DB 5;  Length 91;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db         35 RRC 37


RESULT 16
BQ704626/c
LOCUS       BQ704626                  91 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  Bn01_03123_A
            Bn01_AAFC_ECORC_transgenic_Brassica_napus_overexpressing_BNCBF17_co
            nstitutively_frost_tolerant Brassica napus cDNA clone Bn01_03123,
            mRNA sequence.
ACCESSION   BQ704626
VERSION     BQ704626.1  GI:21844045
KEYWORDS    EST.
SOURCE      Brassica napus (rape)
  ORGANISM  Brassica napus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 91)
  AUTHORS   Singh,J., Allard,G., Tinker,N., Robert,L., Lacroix,C., De Moors,A.,
            Chagnon,J., Farah,S., Couroux,P. and Hattori,J.
  TITLE     Expressed Sequence Tags from constitutively frost tolerant
            transgenic Brassica napus overexpressing BNCBF17
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@agr.gc.ca.
FEATURES             Location/Qualifiers
     source          1. .91
                     /organism="Brassica napus"
                     /mol_type="mRNA"
                     /cultivar="Westar"
                     /db_xref="taxon:3708"
                     /clone="Bn01_03123"
                     /tissue_type="fourth leaf"
                     /dev_stage="3 weeks seedling grown at room temperature"
                     /clone_lib="Bn01_AAFC_ECORC_transgenic_Brassica_napus_over
                     expressing_BNCBF17_constitutively_frost_tolerant"
                     /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
                     Site_2: XhoI; Germinated in soil flats and seedlings grown
                     for 3 weeks in a Conviron E-15 cabinet set at 20oC /16 hr
                     light (250 Em-2sec-1) and 16 oC / 8 hr dark. Fourth leaves
                     collected at 9 am and immediately frozen."
ORIGIN

  Query Match             30.0%;  Score 3;  DB 5;  Length 91;
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYY 9
              |||
Db         37 GYY 35


RESULT 17
AY431374
LOCUS       AY431374                  92 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 36897 unknown mRNA sequence.
ACCESSION   AY431374
VERSION     AY431374.1  GI:42763516
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 92)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 92)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .92
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 36896"
     misc_feature    1. .92
                     /note="unknown; ASAP-UW Feature ID: 36897"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 3;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          7 CWW 9


RESULT 18
AY431374/c
LOCUS       AY431374                  92 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 36897 unknown mRNA sequence.
ACCESSION   AY431374
VERSION     AY431374.1  GI:42763516
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 92)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 92)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .92
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 36896"
     misc_feature    1. .92
                     /note="unknown; ASAP-UW Feature ID: 36897"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 3;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          9 WWG 7


RESULT 19
CNS00YZ0
LOCUS       CNS00YZ0                  93 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN01A02 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL097014
VERSION     AL097014.1  GI:5608625
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
```

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           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1  (bases 1 to 93)
  AUTHORS  Genoscope.
  TITLE    Direct Submission
  JOURNAL  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
           BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
           - Web : www.genoscope.cns.fr)
COMMENT    Determination of this BAC-end sequence was carried out as part of a
           collaboration with the European Drosophila Genome Project (EDGP) -
           http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
           library (Dros BAC) was made by Alain Billaud at CEPH (Centre
           d'Etude du Polymorphisme Humain) with funding provided by a MRC
           project grant. The DNA was prepared from embryos by Alain Bucheton
           and Genevieve Payan. It has been constructed in the vector
           pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .93
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN01A02"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : SP6"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 9;  Length 93;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YYY 10
              |||
Db         70 YYY 72


RESULT 20
CNS00YZ0/c
LOCUS       CNS00YZ0                  93 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
           BACN01A02 of DrosBAC library from Drosophila melanogaster (fruit
           fly), genomic survey sequence.
ACCESSION   AL097014
VERSION     AL097014.1  GI:5608625
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1  (bases 1 to 93)
  AUTHORS  Genoscope.
  TITLE    Direct Submission
  JOURNAL  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
           BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
           - Web : www.genoscope.cns.fr)
COMMENT    Determination of this BAC-end sequence was carried out as part of a
           collaboration with the European Drosophila Genome Project (EDGP) -
           http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
           library (Dros BAC) was made by Alain Billaud at CEPH (Centre
           d'Etude du Polymorphisme Humain) with funding provided by a MRC
           project grant. The DNA was prepared from embryos by Alain Bucheton
           and Genevieve Payan. It has been constructed in the vector
           pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .93
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN01A02"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : SP6"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 9;  Length 93;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RRR 3
              |||
Db         72 RRR 70


RESULT 21
CNS0107O
LOCUS       CNS0107O                  96 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
           BACN03G10 of DrosBAC library from Drosophila melanogaster (fruit
           fly), genomic survey sequence.
ACCESSION   AL098622
VERSION     AL098622.1  GI:5610233
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1  (bases 1 to 96)
  AUTHORS  Genoscope.
  TITLE    Direct Submission
  JOURNAL  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
           BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
           - Web : www.genoscope.cns.fr)
COMMENT    Determination of this BAC-end sequence was carried out as part of a
           collaboration with the European Drosophila Genome Project (EDGP) -
           http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
           library (Dros BAC) was made by Alain Billaud at CEPH (Centre
           d'Etude du Polymorphisme Humain) with funding provided by a MRC
           project grant. The DNA was prepared from embryos by Alain Bucheton
           and Genevieve Payan. It has been constructed in the vector
           pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .96
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN03G10"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN

  Query Match           30.0%;  Score 3;  DB 9;  Length 96;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WWG 7
              |||
Db          2 WWG 4


RESULT 22
CNS0107O/c
LOCUS       CNS0107O                  96 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
           BACN03G10 of DrosBAC library from Drosophila melanogaster (fruit
           fly), genomic survey sequence.
ACCESSION   AL098622
VERSION     AL098622.1  GI:5610233
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Ephydroidea; Drosophilidae; Drosophila.
```

```
REFERENCE   1  (bases 1 to 96)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .96
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN03G10"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 9;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CWW 6
              |||
Db          4 CWW 2


RESULT 23
CNS0429N
LOCUS       CNS0429N                  98 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            075N24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL271220
VERSION     AL271220.1  GI:7993184
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 98)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .98
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="075N24"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG075DG12LP1~end : T7"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 9;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 RRC 4
              |||
Db          8 RRC 10


RESULT 24
CNS0429N/c
LOCUS       CNS0429N                  98 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            075N24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL271220
VERSION     AL271220.1  GI:7993184
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 98)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .98
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="075N24"
                     /clone_lib="G"
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                     /note="Genoscope sequence ID : C0BG075DG12LP1~end : T7"
ORIGIN

  Query Match             30.0%;  Score 3;  DB 9;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GYY 9
              |||
Db         10 GYY 8


RESULT 25
CNS00I17
LOCUS       CNS00I17                  25 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR36J06 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL074604
VERSION     AL074604.1  GI:4953980
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR36J06"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db          6 RC 7


RESULT 26
CNS00I17/c
LOCUS       CNS00I17                  25 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR36J06 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL074604
VERSION     AL074604.1  GI:4953980
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 25)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .25
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR36J06"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db          7 GY 6


RESULT 27
CNS00C45
LOCUS       CNS00C45                  30 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR25K03 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL058402
VERSION     AL058402.1  GI:4946279
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
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            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR25K03"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         26 CW 27


RESULT 28
CNS00C45/c
LOCUS       CNS00C45                  30 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR25K03 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL058402
VERSION     AL058402.1  GI:4946279
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 30)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .30
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR25K03"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         27 WG 26


RESULT 29
CNS00JBW
LOCUS       CNS00JBW                  36 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR38L23 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL075982
VERSION     AL075982.1  GI:4955661
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .36
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR38L23"
                     /clone_lib="RPCI-98"
                     /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         27 RC 28


RESULT 30
CNS00JBW/c
LOCUS       CNS00JBW                  36 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR38L23 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL075982
VERSION     AL075982.1  GI:4955661
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
```

```
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 36)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .36
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR38L23"
                      /clone_lib="RPCI-98"
                      /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 36;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         28 GY 27


RESULT 31
CNS00L8C
LOCUS       CNS00L8C                  38 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR24P20 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL068197
VERSION     AL068197.1  GI:4958134
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .38
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR24P20"
                      /clone_lib="RPCI-98"
                      /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         22 RC 23


RESULT 32
CNS00L8C/c
LOCUS       CNS00L8C                  38 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR24P20 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL068197
VERSION     AL068197.1  GI:4958134
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .38
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR24P20"
                      /clone_lib="RPCI-98"
                      /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          7 GY 8
              ||
Db         27 GY 26


RESULT 33
AW059591
LOCUS       AW059591                 41 bp    mRNA    linear   EST 23-AUG-2000
DEFINITION  HuTH.bsst.dnc15.final.cluster_81_(3) DNC15 Homo sapiens cDNA
            similar to LD78, mRNA sequence.
ACCESSION   AW059591
VERSION     AW059591.1  GI:6651913
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
            McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
            Burcham,T. and Albrecht,G.
  TITLE     In vitro cloning of complex mixtures of DNA on microbeads: Physical
            separation of differentially expressed cDNAs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
  MEDLINE   20144098
   PUBMED   10677516
COMMENT     Contact: Burcham TS
            LYNX Therapeutics, Inc.
            25861 Industrial Blvd., Hayward, CA 94545, USA
            Tel: 510 670 9338
            Fax: 510 670 9302
            Email: timb@lynxgen.com
            Sequence obtained from LYNX Therapeutics Megasort technology.
            Collected from the down-regulated gate. Consensus sequence of 3
            sequences in cluster.
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocyctic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="DNC15"
                     /note="Vector: pCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of down-regulated cDNA. THP-1
                     cells non-induced (treated with DMSO only). "
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         14 RC 15


RESULT 34
AW059591/c
LOCUS       AW059591                 41 bp    mRNA    linear   EST 23-AUG-2000
DEFINITION  HuTH.bsst.dnc15.final.cluster_81_(3) DNC15 Homo sapiens cDNA
            similar to LD78, mRNA sequence.
ACCESSION   AW059591
VERSION     AW059591.1  GI:6651913
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
            McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
            Burcham,T. and Albrecht,G.
  TITLE     In vitro cloning of complex mixtures of DNA on microbeads: Physical
            separation of differentially expressed cDNAs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
  MEDLINE   20144098
   PUBMED   10677516
COMMENT     Contact: Burcham TS
            LYNX Therapeutics, Inc.
            25861 Industrial Blvd., Hayward, CA 94545, USA
            Tel: 510 670 9338
            Fax: 510 670 9302
            Email: timb@lynxgen.com
            Sequence obtained from LYNX Therapeutics Megasort technology.
            Collected from the down-regulated gate. Consensus sequence of 3
            sequences in cluster.
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocyctic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="DNC15"
                     /note="Vector: pCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of down-regulated cDNA. THP-1
                     cells non-induced (treated with DMSO only). "
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         15 GY 14


RESULT 35
AW059842
LOCUS       AW059842                 41 bp    mRNA    linear   EST 23-AUG-2000
DEFINITION  HuTH.bsst.upc15.final.cluster_1_(363) UPC15 Homo sapiens cDNA
            similar to MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA, mRNA sequence.
ACCESSION   AW059842
VERSION     AW059842.1  GI:6652164
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
            McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
            Burcham,T. and Albrecht,G.
  TITLE     In vitro cloning of complex mixtures of DNA on microbeads: Physical
            separation of differentially expressed cDNAs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
  MEDLINE   20144098
   PUBMED   10677516
COMMENT     Contact: Burcham TS
            LYNX Therapeutics, Inc.
            25861 Industrial Blvd., Hayward, CA 94545, USA
            Tel: 510 670 9338
            Fax: 510 670 9302
            Email: timb@lynxgen.com
            Sequence obtained from LYNX Therapeutics Megasort technology.
            Collected from the up-regulated gate. Consensus sequence of 363
            sequences in cluster.
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocyctic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="UPC15"
                     /note="Vector: pCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of up-regulated cDNA. THP-1
                     cells induced with 100 nM PMA in DMSO. "
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         27 GY 28


RESULT 36
AW059842/c
LOCUS       AW059842                41 bp    mRNA    linear   EST 23-AUG-2000
DEFINITION  HuTH.bsst.upc15.final.cluster_1_(363) UPC15 Homo sapiens cDNA
            similar to MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA, mRNA sequence.
ACCESSION   AW059842
VERSION     AW059842.1  GI:6652164
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
            McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
            Burcham,T. and Albrecht,G.
  TITLE     In vitro cloning of complex mixtures of DNA on microbeads: Physical
            separation of differentially expressed cDNAs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
  MEDLINE   20144098
   PUBMED   10677516
COMMENT     Contact: Burcham TS
            LYNX Therapeutics, Inc.
            25861 Industrial Blvd., Hayward, CA 94545, USA
            Tel: 510 670 9338
            Fax: 510 670 9302
            Email: timb@lynxgen.com
            Sequence obtained from LYNX Therapeutics Megasort technology.
            Collected from the up-regulated gate. Consensus sequence of 363
            sequences in cluster.
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
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                     /db_xref="taxon:9606"
                     /cell_type="monocyctic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="UPC15"
                     /note="Vector: pCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of up-regulated cDNA. THP-1
                     cells induced with 100 nM PMA in DMSO. "
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
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Db         28 RC 27


RESULT 37
AW059847
LOCUS       AW059847                41 bp    mRNA    linear   EST 23-AUG-2000
DEFINITION  HuTH.bsst.upc15.final.cluster_6_(24) UPC15 Homo sapiens cDNA
            similar to MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA, mRNA sequence.
ACCESSION   AW059847
VERSION     AW059847.1  GI:6652169
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
            McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
            Burcham,T. and Albrecht,G.
  TITLE     In vitro cloning of complex mixtures of DNA on microbeads: Physical
            separation of differentially expressed cDNAs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
  MEDLINE   20144098
   PUBMED   10677516
COMMENT     Contact: Burcham TS
            LYNX Therapeutics, Inc.
            25861 Industrial Blvd., Hayward, CA 94545, USA
            Tel: 510 670 9338
            Fax: 510 670 9302
            Email: timb@lynxgen.com
            Sequence obtained from LYNX Therapeutics Megasort technology.
            Collected from the up-regulated gate. Consensus sequence of 24
            sequences in cluster.
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocyctic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="UPC15"
                     /note="Vector: pCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of up-regulated cDNA. THP-1
                     cells induced with 100 nM PMA in DMSO. "
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         40 GY 41


RESULT 38
AW059847/c
LOCUS       AW059847                41 bp    mRNA    linear   EST 23-AUG-2000
DEFINITION  HuTH.bsst.upc15.final.cluster_6_(24) UPC15 Homo sapiens cDNA
            similar to MACROPHAGE INFLAMMATORY PROTEIN 1-ALPHA, mRNA sequence.
ACCESSION   AW059847
VERSION     AW059847.1  GI:6652169
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
            McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
            Burcham,T. and Albrecht,G.
  TITLE     In vitro cloning of complex mixtures of DNA on microbeads: Physical
            separation of differentially expressed cDNAs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
  MEDLINE   20144098
   PUBMED   10677516
```

```
COMMENT     Contact: Burcham TS
            LYNX Therapeutics, Inc.
            25861 Industrial Blvd., Hayward, CA 94545, USA
            Tel: 510 670 9338
            Fax: 510 670 9302
            Email: timb@lynxgen.com
            Sequence obtained from LYNX Therapeutics Megasort technology.
            Collected from the up-regulated gate. Consensus sequence of 24
            sequences in cluster.
            High quality sequence stop: 41.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocyctic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="UPC15"
                     /note="Vector: pCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of up-regulated cDNA. THP-1
                     cells induced with 100 nM PMA in DMSO. "
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         41 RC 40


RESULT 39
CNS00COP
LOCUS       CNS00COP                  41 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR26A10 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL059445
VERSION     AL059445.1  GI:4947009
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR26A10"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         37 CW 38


RESULT 40
CNS00COP/c
LOCUS       CNS00COP                  41 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR26A10 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL059445
VERSION     AL059445.1  GI:4947009
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 41)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .41
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR26A10"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 41;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         39 CW 38


RESULT 41
CNS00COG
LOCUS       CNS00COG                  43 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR26P07 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
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ACCESSION   AL059436
VERSION     AL059436.1  GI:4947000
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR26P07"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         38 GY 39


RESULT 42
CNS00COG/c
LOCUS       CNS00COG                  43 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR26P07 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL059436
VERSION     AL059436.1  GI:4947000
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 43)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .43
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR26P07"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 43;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         39 RC 38


RESULT 43
CN813621
LOCUS       CN813621                  45 bp    mRNA    linear   EST 01-JUN-2004
DEFINITION  Fg06_02107_A Fg06_AAFC_ECORC_Fusarium_graminearum_perithecia
            Gibberella zeae cDNA clone Fg06_02107, mRNA sequence.
ACCESSION   CN813621
VERSION     CN813621.1  GI:47837632
KEYWORDS    EST.
SOURCE      Gibberella zeae (anamorph: Fusarium graminearum)
  ORGANISM  Gibberella zeae
            Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
            Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE   1  (bases 1 to 45)
  AUTHORS   Harris,L.J., Rocheleau,H., Ouellet,T., Allard,S., Chapados,J.,
            Couroux,P., De Moors,A., Hattori,J.I., Lacroix,C., Masotti,M.,
            Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.
  TITLE     Expressed Sequence Tags from Fusarium graminearum enriched for late
            stage perithecia
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Harris, Linda J.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
            CANADA
            Tel: (613) 759-1314
            Fax: (613) 759-6566
            Email: harrislj@agr.gc.ca.
FEATURES             Location/Qualifiers
     source          1. .45
                     /organism="Gibberella zeae"
                     /mol_type="mRNA"
                     /strain="DAOM 180378"
                     /db_xref="taxon:5518"
                     /clone="Fg06_02107"
                     /dev_stage="Sexual"
                     /lab_host="E. coli DH10B"
                     /clone_lib="Fg06_AAFC_ECORC_Fusarium_graminearum_peritheci
                     a"
                     /note="Vector: pGem-T easy; Site_1: EcoRI; Mycelia grown
                     on carrot agar at 20oC until confluent; perithecia induced
                     with Tween 40 solution (25% v/v). Fruiting bodies were
                     collected 20 days after induction. Total RNA was extracted
                     using Trizol. cDNAs were amplified using Invitrogen
                     GeneRacer kit. cDNA was not fractionated and was
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bidirectionally cloned."
ORIGIN

Query Match 20.0%; Score 2; DB 7; Length 45;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
||
Db 11 CW 12

RESULT 44
CN813621/c
LOCUS CN813621 45 bp mRNA linear EST 01-JUN-2004
DEFINITION Fg06_02107_A Fg06_AAFC_ECORC_Fusarium_graminearum_perithecia Gibberella zeae cDNA clone Fg06_02107, mRNA sequence.
ACCESSION CN813621
VERSION CN813621.1 GI:47837632
KEYWORDS EST.
SOURCE Gibberella zeae (anamorph: Fusarium graminearum)
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 45)
AUTHORS Harris,L.J., Rocheleau,H., Ouellet,T., Allard,S., Chapados,J., Couroux,P., De Moors,A., Hattori,J.I., Lacroix,C., Masotti,M., Robert,L.S., Singh,J.A., Sprott,D. and Tinker,N.A.
TITLE Expressed Sequence Tags from Fusarium graminearum enriched for late stage perithecia
JOURNAL Unpublished (2004)
COMMENT Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6, CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrislj@agr.gc.ca.
FEATURES Location/Qualifiers
source 1. .45
/organism="Gibberella zeae"
/mol_type="mRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg06_02107"
/dev_stage="Sexual"
/lab_host="E. coli DH10B"
/clone_lib="Fg06_AAFC_ECORC_Fusarium_graminearum_perithecia"
/note="Vector: pGem-T easy; Site_1: EcoRI; Mycelia grown on carrot agar at 20oC until confluent; perithecia induced with Tween 40 solution (25% v/v). Fruiting bodies were collected 20 days after induction. Total RNA was extracted using Trizol. cDNAs were amplified using Invitrogen GeneRacer kit. cDNA was not fractionated and was bidirectionally cloned."
ORIGIN

Query Match 20.0%; Score 2; DB 7; Length 45;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
||
Db 12 WG 11

RESULT 45
AW059540
LOCUS AW059540 47 bp mRNA linear EST 23-AUG-2000
DEFINITION HuTH.bsst.dnc15.final.cluster_17_(10) DNC15 Homo sapiens cDNA similar to catalase, mRNA sequence.
ACCESSION AW059540
VERSION AW059540.1 GI:6651850
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 47)
AUTHORS Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B., Burcham,T. and Albrecht,G.
TITLE In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
MEDLINE 20144098
PUBMED 10677516
COMMENT Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338
Fax: 510 670 9302
Email: timb@lynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the down-regulated gate. Consensus sequence of 10 sequences in cluster.
High quality sequence stop: 47.
FEATURES Location/Qualifiers
source 1. .47
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="monocyctic leukemia"
/cell_line="THP-1 (TIB-202)"
/clone_lib="DNC15"
/note="Vector: pCR2.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only). "
ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4
||
Db 1 RC 2

RESULT 46
AW059540/c
LOCUS AW059540 47 bp mRNA linear EST 23-AUG-2000
DEFINITION HuTH.bsst.dnc15.final.cluster_17_(10) DNC15 Homo sapiens cDNA similar to catalase, mRNA sequence.
ACCESSION AW059540
VERSION AW059540.1 GI:6651850
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 47)
AUTHORS Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K., McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B., Burcham,T. and Albrecht,G.
TITLE In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
MEDLINE 20144098
PUBMED 10677516
COMMENT Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338

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            Fax: 510 670 9302
            Email: timb@lynxgen.com
            Sequence obtained from LYNX Therapeutics Megasort technology.
            Collected from the down-regulated gate. Consensus sequence of 10
            sequences in cluster.
            High quality sequence stop: 47.
FEATURES              Location/Qualifiers
     source           1. .47
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /cell_type="monocyctic leukemia"
                      /cell_line="THP-1 (TIB-202)"
                      /clone_lib="DNC15"
                      /note="Vector: pCR2.1; Cloning of PCR products from
                      micro-beads carrying 3' end of down-regulated cDNA. THP-1
                      cells non-induced (treated with DMSO only). "
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 47;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
            ||
Db          2 GY 1


RESULT 47
CNS00J6U
LOCUS       CNS00J6U                  48 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR38C14 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL075800
VERSION     AL075800.1  GI:4955479
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .48
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR38C14"
                      /clone_lib="RPCI-98"
                      /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
            ||
Db         35 GY 36


RESULT 48
CNS00J6U/c
LOCUS       CNS00J6U                  48 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR38C14 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL075800
VERSION     AL075800.1  GI:4955479
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 48)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .48
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR38C14"
                      /clone_lib="RPCI-98"
                      /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 48;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
            ||
Db         36 RC 35


RESULT 49
AW496816
LOCUS       AW496816                  49 bp    mRNA    linear   EST 01-MAR-2000
DEFINITION  1cj Neuronal Differentiation of the NT2/D1 cell line. Homo sapiens
            cDNA 3' similar to ubiquitin-protein ligase E3-alpha (UBR1), mRNA
            sequence.
ACCESSION   AW496816
VERSION     AW496816.1  GI:7118839
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Bevort,M.
  TITLE     Analysis of gene expression during neuronal differentiation of
            NT2/D1 cells
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Bevort M
            Department of Growth and Reproduction GR-5064
            Copenhagen University Hospital
            Blegdamsvej 9, 2100 Copenhagen, Denmark
            Tel: +45 35455081
            Fax: +45 35456054
            Email: maja@biobase.dk
            The EST is up regulated, during neuronal differentiation of the
            NT2/D1 cell line (replated fully differentiated neurones not
            analysed).
            PCR PRimers
            FORWARD: CCAATCCCCAGTT
            BACKWARD: AAGCTTTTTTTTTTTG
            Seq primer: T7, CY5-TAATACGACTCACTATAGGGCC
            High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="NT2/D1"
                     /clone_lib="Neuronal Differentiation of the NT2/D1 cell
                     line."
                     /note="The EST is derived from direct sequencing of a
                     Differential  Display fragment. Laboratory manuals are
                     available from  http//www.biobase.dk/~ddbase"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db          2 CW 3


RESULT 50
AW496816/c
LOCUS       AW496816                49 bp    mRNA    linear   EST 01-MAR-2000
DEFINITION  1cj Neuronal Differentiation of the NT2/D1 cell line. Homo sapiens
            cDNA 3' similar to ubiquitin-protein ligase E3-alpha (UBR1), mRNA
            sequence.
ACCESSION   AW496816
VERSION     AW496816.1  GI:7118839
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 49)
  AUTHORS   Bevort,M.
  TITLE     Analysis of gene expression during neuronal differentiation of
            NT2/D1 cells
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Bevort M
            Department of Growth and Reproduction GR-5064
            Copenhagen University Hospital
            Blegdamsvej 9, 2100 Copenhagen, Denmark
            Tel: +45 35455081
            Fax: +45 35456054
            Email: maja@biobase.dk
            The EST is up regulated, during neuronal differentiation of the
            NT2/D1 cell line (replated fully differentiated neurones not
            analysed).
            PCR PRimers
            FORWARD: CCAATCCCCAGTT
            BACKWARD: AAGCTTTTTTTTTTTG
            Seq primer: T7, CY5-TAATACGACTCACTATAGGGCC
            High quality sequence stop: 49.
FEATURES             Location/Qualifiers
     source          1. .49
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="NT2/D1"
                     /clone_lib="Neuronal Differentiation of the NT2/D1 cell
                     line."
                     /note="The EST is derived from direct sequencing of a
                     Differential  Display fragment. Laboratory manuals are
                     available from  http//www.biobase.dk/~ddbase"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db          3 WG 2


RESULT 51
CNS00AWB
LOCUS       CNS00AWB                50 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR22A09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL056017
VERSION     AL056017.1  GI:4936887
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR22A09"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 50;
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         18 GY 19


RESULT 52
CNS00AWB/c
LOCUS       CNS00AWB                   50 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR22A09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL056017
VERSION     AL056017.1  GI:4936887
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .50
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACR22A09"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 50;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         45 RC 44


RESULT 53
AW444398
LOCUS       AW444398                   51 bp    mRNA    linear   EST 25-SEP-2000
DEFINITION  AB558 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA
            sequence.
ACCESSION   AW444398
VERSION     AW444398.1  GI:10282196
KEYWORDS    EST.
SOURCE      Agaricus bisporus
  ORGANISM  Agaricus bisporus
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
            Agaricales; Agaricaceae; Agaricus.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.
  TITLE     Classification of sequences expressed during the primordial and
            basidiome stages of the cultivated mushroom Agaricus bisporus
  JOURNAL   Fungal Genet. Biol. 29 (2), 81-94 (2000)
  MEDLINE   20374017
   PUBMED   10919377
COMMENT     Contact: Manuel D. Ospina-Giraldo
            Mushroom Research Laboratory, Department of Plant Pathology
            The Pennsylvania State University
            305 Buckhout, University Park, PA 16802, USA
            Tel: 8148633073
            Fax: 8148637217
            Email: mxo11@psu.edu
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Agaricus bisporus"
                     /mol_type="mRNA"
                     /strain="Sylvan-130"
                     /db_xref="taxon:5341"
                     /tissue_type="Primordium"
                     /clone_lib="Primordium cDNA library"
                     /note="Vector: pBluescript II SK (+); Site_1: SalI;
                     Site_2: NotI"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         36 GY 37


RESULT 54
AW444398/c
LOCUS       AW444398                   51 bp    mRNA    linear   EST 25-SEP-2000
DEFINITION  AB558 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA
            sequence.
ACCESSION   AW444398
VERSION     AW444398.1  GI:10282196
KEYWORDS    EST.
SOURCE      Agaricus bisporus
  ORGANISM  Agaricus bisporus
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
            Agaricales; Agaricaceae; Agaricus.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.
  TITLE     Classification of sequences expressed during the primordial and
            basidiome stages of the cultivated mushroom Agaricus bisporus
  JOURNAL   Fungal Genet. Biol. 29 (2), 81-94 (2000)
  MEDLINE   20374017
   PUBMED   10919377
COMMENT     Contact: Manuel D. Ospina-Giraldo
            Mushroom Research Laboratory, Department of Plant Pathology
            The Pennsylvania State University
            305 Buckhout, University Park, PA 16802, USA
            Tel: 8148633073
            Fax: 8148637217
            Email: mxo11@psu.edu
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Agaricus bisporus"
                     /mol_type="mRNA"
                     /strain="Sylvan-130"
                     /db_xref="taxon:5341"
                     /tissue_type="Primordium"
                     /clone_lib="Primordium cDNA library"
                     /note="Vector: pBluescript II SK (+); Site_1: SalI;
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```
                    Site_2: NotI"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         37 RC 36


RESULT 55
CNS00BFG
LOCUS       CNS00BFG                  51 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR23P07 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL057009
VERSION     AL057009.1  GI:4937576
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .51
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR23P07"
                      /clone_lib="RPCI-98"
                      /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         34 RC 35


RESULT 56
CNS00BFG/c
LOCUS       CNS00BFG                  51 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR23P07 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL057009
VERSION     AL057009.1  GI:4937576
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .51
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR23P07"
                      /clone_lib="RPCI-98"
                      /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         35 GY 34


RESULT 57
CNS00IH3
LOCUS       CNS00IH3                  51 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR36D06 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL074772
VERSION     AL074772.1  GI:4954552
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
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            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .51
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR36D06"
                      /clone_lib="RPCI-98"
                      /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         36 RC 37


RESULT 58
CNS00IH3/c
LOCUS       CNS00IH3                  51 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR36D06 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL074772
VERSION     AL074772.1  GI:4954552
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .51
                      /organism="Drosophila melanogaster"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:7227"
                      /clone="BACR36D06"
                      /clone_lib="RPCI-98"
                      /note="end : TET3"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         37 GY 36


RESULT 59
CNS02CBU
LOCUS       CNS02CBU                  51 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            255I13 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL190947
VERSION     AL190947.1  GI:7829051
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 51)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES              Location/Qualifiers
     source           1. .51
                      /organism="Tetraodon nigroviridis"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:99883"
                      /clone="255I13"
                      /clone_lib="G"
                      /note="Genoscope sequence ID : C0AG255AE07SP1~end :
                      PUC-Ori"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         10 CW 11


RESULT 60
```

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CNS02CBU/c
LOCUS       CNS02CBU                  51 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            255I13 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL190947
VERSION     AL190947.1  GI:7829051
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 51)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .51
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="255I13"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG255AE07SP1~end :
                     PUC-Ori"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         11 WG 10


RESULT 61
AW582795
LOCUS       AW582795                  52 bp    mRNA    linear   EST 01-APR-2000
DEFINITION  1sm Neuronal Differentiation of the NT2/D1 cell line. Homo sapiens
            cDNA 3' similar to EST, mRNA sequence.
ACCESSION   AW582795
VERSION     AW582795.1  GI:7382041
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Bevort,M.
  TITLE     Analysis of gene expression during neuronal differentiation of
            NT2/D1 cells
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Bevort M
            Department of Growth and Reproduction GR-5064
            Copenhagen University Hospital
            Blegdamsvej 9, 2100 Copenhagen, Denmark
            Tel: +45 35455081
            Fax: +45 35456054
            Email: maja@biobase.dk
            The EST is up regulated, during neuronal differentiation of the
            NT2/ D1 cell line (replated fully differentiated neurone s not
            analysed).
            PCR PRimers
            FORWARD: TGACGAGGTGTCT
            BACKWARD: AAGCTTTTTTTTTTTC
            Seq primer: T7, CY5-TAATACGACTCACTATAGGGCC
            High quality sequence stop: 52.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="NT2/D1"
                     /clone_lib="Neuronal Differentiation of the NT2/D1 cell
                     line."
                     /note="The EST is derived from direct sequencing of a
                     Differential  Display fragment. Laboratory manuals are
                     available from  http//www.biobase.dk/~ddbase"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         22 CW 23


RESULT 62
AW582795/c
LOCUS       AW582795                  52 bp    mRNA    linear   EST 01-APR-2000
DEFINITION  1sm Neuronal Differentiation of the NT2/D1 cell line. Homo sapiens
            cDNA 3' similar to EST, mRNA sequence.
ACCESSION   AW582795
VERSION     AW582795.1  GI:7382041
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Bevort,M.
  TITLE     Analysis of gene expression during neuronal differentiation of
            NT2/D1 cells
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Bevort M
            Department of Growth and Reproduction GR-5064
            Copenhagen University Hospital
            Blegdamsvej 9, 2100 Copenhagen, Denmark
            Tel: +45 35455081
            Fax: +45 35456054
            Email: maja@biobase.dk
            The EST is up regulated, during neuronal differentiation of the
            NT2/ D1 cell line (replated fully differentiated neurone s not
            analysed).
            PCR PRimers
            FORWARD: TGACGAGGTGTCT
            BACKWARD: AAGCTTTTTTTTTTTC
```

```
            Seq primer: T7, CY5-TAATACGACTCACTATAGGGCC
            High quality sequence stop: 52.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="NT2/D1"
                     /clone_lib="Neuronal Differentiation of the NT2/D1 cell
                     line."
                     /note="The EST is derived from direct sequencing of a
                     Differential  Display fragment. Laboratory manuals are
                     available from  http//www.biobase.dk/~ddbase"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         23 WG 22


RESULT 63
CNS0102A
LOCUS       CNS0102A                  52 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN03D23 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL098428
VERSION     AL098428.1  GI:5610039
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN03D23"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         30 RC 31


RESULT 64
CNS0102A/c
LOCUS       CNS0102A                  52 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN03D23 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL098428
VERSION     AL098428.1  GI:5610039
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .52
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN03D23"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         31 GY 30


RESULT 65
CNS011OZ
LOCUS       CNS011OZ                  52 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN06F24 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL100541
VERSION     AL100541.1  GI:5612152
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
```

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            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES                Location/Qualifiers
     source             1. .52
                        /organism="Drosophila melanogaster"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:7227"
                        /clone="BACN06F24"
                        /clone_lib="DrosBAC"
                        /plasmid="pBeloBAC11"
                        /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         29 CW 30


RESULT 66
CNS011OZ/c
LOCUS       CNS011OZ                  52 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN06F24 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL100541
VERSION     AL100541.1  GI:5612152
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES                Location/Qualifiers
     source             1. .52
                        /organism="Drosophila melanogaster"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:7227"
                        /clone="BACN06F24"
                        /clone_lib="DrosBAC"
                        /plasmid="pBeloBAC11"
                        /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         30 WG 29


RESULT 67
CNS011VR
LOCUS       CNS011VR                  52 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN06E01 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL100785
VERSION     AL100785.1  GI:5612396
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES                Location/Qualifiers
     source             1. .52
                        /organism="Drosophila melanogaster"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:7227"
                        /clone="BACN06E01"
                        /clone_lib="DrosBAC"
                        /plasmid="pBeloBAC11"
                        /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         35 CW 36


RESULT 68
CNS011VR/c
LOCUS       CNS011VR                  52 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN06E01 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL100785
VERSION     AL100785.1  GI:5612396
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 52)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
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FEATURES             Location/Qualifiers
     source          1. .52
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN06E01"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN

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Qy          4 CW 5
              ||
Db          3 CW 2


RESULT 69
AY432321
LOCUS       AY432321                  53 bp    mRNA    linear   HTC 23-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 36043 unknown mRNA sequence.
ACCESSION   AY432321
VERSION     AY432321.1  GI:42762493
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 53)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 36042"
     misc_feature    1. .53
                     /note="unknown; ASAP-UW Feature ID: 36043"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db          6 CW 7


RESULT 70
AY432321/c
LOCUS       AY432321                  53 bp    mRNA    linear   HTC 23-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 36043 unknown mRNA sequence.
ACCESSION   AY432321
VERSION     AY432321.1  GI:42762493
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 53)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 36042"
     misc_feature    1. .53
                     /note="unknown; ASAP-UW Feature ID: 36043"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
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Db          7 WG 6
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RESULT 71
AY440477
LOCUS       AY440477                  53 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Armigeres subalbatus ASAP ID: 41399 unknown mRNA sequence.
ACCESSION   AY440477
VERSION     AY440477.1  GI:42765506
KEYWORDS    HTC.
SOURCE      Armigeres subalbatus
  ORGANISM  Armigeres subalbatus
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Armigeres.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 53)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="Armigeres subalbatus"
                     /mol_type="mRNA"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:124917"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 41398"
     misc_feature    1. .53
                     /note="unknown; low quality sequence; ASAP-UW Feature ID:
                     41399"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
               ||
Db          5 GY 6


RESULT 72
AY440477/c
LOCUS       AY440477                  53 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Armigeres subalbatus ASAP ID: 41399 unknown mRNA sequence.
ACCESSION   AY440477
VERSION     AY440477.1  GI:42765506
KEYWORDS    HTC.
SOURCE      Armigeres subalbatus
  ORGANISM  Armigeres subalbatus
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Armigeres.
REFERENCE   1  (bases 1 to 53)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 53)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="Armigeres subalbatus"
                     /mol_type="mRNA"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:124917"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 41398"
     misc_feature    1. .53
                     /note="unknown; low quality sequence; ASAP-UW Feature ID:
                     41399"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
               ||
Db          6 RC 5


RESULT 73
CNS02YBO
LOCUS       CNS02YBO                  53 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            180E24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL219453
VERSION     AL219453.1  GI:7878272
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
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            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 53)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="180E24"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG180BC12SP1~end :
                     PUC-Ori"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         36 CW 37


RESULT 74
CNS02YBO/c
LOCUS       CNS02YBO                  53 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            180E24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL219453
VERSION     AL219453.1  GI:7878272
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 53)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .53
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="180E24"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG180BC12SP1~end :
                     PUC-Ori"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         37 WG 36


RESULT 75
AY431290
LOCUS       AY431290                  54 bp    mRNA    linear   HTC 23-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 38199 unknown mRNA sequence.
ACCESSION   AY431290
VERSION     AY431290.1  GI:42762176
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 54)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
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                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 38198"
     misc_feature    1. .54
                     /note="unknown; ASAP-UW Feature ID: 38199"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         50 CW 51


RESULT 76
AY431290/c
LOCUS       AY431290                54 bp    mRNA    linear   HTC 23-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 38199 unknown mRNA sequence.
ACCESSION   AY431290
VERSION     AY431290.1  GI:42762176
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 54)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 54)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .54
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 38198"
     misc_feature    1. .54
                     /note="unknown; ASAP-UW Feature ID: 38199"
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  Query Match             20.0%;  Score 2;  DB 3;  Length 54;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db          4 CW 3


RESULT 77
AW497627
LOCUS       AW497627                55 bp    mRNA    linear   EST 01-MAR-2000
DEFINITION  rps7g2b81 Neuronal Differentiation of the NT2/D1 cell line. Homo
            sapiens cDNA 3', mRNA sequence.
ACCESSION   AW497627
VERSION     AW497627.1  GI:7119224
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Bevort,M.
  TITLE     Analysis of gene expression during neuronal differentiation of
            NT2/D1 cells
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Bevort M
            Department of Growth and Reproduction GR-5064
            Copenhagen University Hospital
            Blegdamsvej 9, 2100 Copenhagen, Denmark
            Tel: +45 35455081
            Fax: +45 35456054
            Email: maja@biobase.dk
            The EST's expression level is constant, during neuronal
            differentiation of the NT2/D1 cell line.
            PCR PRimers
            FORWARD: GCCCACATAACCATG
            BACKWARD: AAGCTTTTTTTTTTG
            Seq primer: T7, CY5-TAATACGACTCACTATAGGGCC
            High quality sequence stop: 55.
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="NT2/D1"
                     /clone_lib="Neuronal Differentiation of the NT2/D1 cell
                     line."
                     /note="The EST is derived from direct sequencing of a
                     Differential  Display fragment. Laboratory manuals are
                     available from  http//www.biobase.dk/~ddbase"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         17 WG 18


RESULT 78
AW497627/c
LOCUS       AW497627                55 bp    mRNA    linear   EST 01-MAR-2000
DEFINITION  rps7g2b81 Neuronal Differentiation of the NT2/D1 cell line. Homo
            sapiens cDNA 3', mRNA sequence.
ACCESSION   AW497627
VERSION     AW497627.1  GI:7119224
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KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 55)
  AUTHORS   Bevort,M.
  TITLE     Analysis of gene expression during neuronal differentiation of
            NT2/D1 cells
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Bevort M
            Department of Growth and Reproduction GR-5064
            Copenhagen University Hospital
            Blegdamsvej 9, 2100 Copenhagen, Denmark
            Tel: +45 35455081
            Pax: +45 35456054
            Email: maja@biobase.dk
            The EST's expression level is constant, during neuronal
            differentiation of the NT2/D1 cell line.
            PCR PRimers
            FORWARD: GCCCACATAACCATG
            BACKWARD: AAGCTTTTTTTTTTG
            Seq primer: T7, CY5-TAATACGACTCACTATAGGGCC
            High quality sequence stop: 55.
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="NT2/D1"
                     /clone_lib="Neuronal Differentiation of the NT2/D1 cell
                     line."
                     /note="The EST is derived from direct sequencing of a
                     Differential  Display fragment. Laboratory manuals are
                     available from  http//www.biobase.dk/~ddbase"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         18 CW 17


RESULT 79
CNS025NE
LOCUS       CNS025NE                   55 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            238C04 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL182291
VERSION     AL182291.1  GI:7820389
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 55)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="238C04"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG238BB02SP1-end :
                     PUC-Ori"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         33 RC 34


RESULT 80
CNS025NE/c
LOCUS       CNS025NE                   55 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            238C04 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL182291
VERSION     AL182291.1  GI:7820389
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 55)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
```

```
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .55
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="238C04"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG238BB02SP1~end :
                     PUC-Ori"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 55;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         34 GY 33


RESULT 81
AW444238
LOCUS       AW444238                  56 bp    mRNA    linear   EST 25-SEP-2000
DEFINITION  AB562 Basidiome cDNA library Agaricus bisporus cDNA 5', mRNA
            sequence.
ACCESSION   AW444238
VERSION     AW444238.1  GI:10282036
KEYWORDS    EST.
SOURCE      Agaricus bisporus
  ORGANISM  Agaricus bisporus
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
            Agaricales; Agaricaceae; Agaricus.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.
  TITLE     Classification of sequences expressed during the primordial and
            basidiome stages of the cultivated mushroom Agaricus bisporus
  JOURNAL   Fungal Genet. Biol. 29 (2), 81-94 (2000)
  MEDLINE   20374017
   PUBMED   10919377
COMMENT     Contact: Manuel D. Ospina-Giraldo
            Mushroom Research Laboratory, Department of Plant Pathology
            The Pennsylvania State University
            305 Buckhout, University Park, PA 16802, USA
            Tel: 8148633073
            Fax: 8148637217
            Email: mxo11@psu.edu
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .56
                     /organism="Agaricus bisporus"
                     /mol_type="mRNA"
                     /strain="Sylvan-130"
                     /db_xref="taxon:5341"
                     /tissue_type="Basidiome"
                     /clone_lib="Basidiome cDNA library"
                     /note="Vector: pBluescript II SK (+); Site_1: SalI;
                     Site_2: NotI"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         11 WG 12


RESULT 82
AW444238/c
LOCUS       AW444238                  56 bp    mRNA    linear   EST 25-SEP-2000
DEFINITION  AB562 Basidiome cDNA library Agaricus bisporus cDNA 5', mRNA
            sequence.
ACCESSION   AW444238
VERSION     AW444238.1  GI:10282036
KEYWORDS    EST.
SOURCE      Agaricus bisporus
  ORGANISM  Agaricus bisporus
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
            Agaricales; Agaricaceae; Agaricus.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.
  TITLE     Classification of sequences expressed during the primordial and
            basidiome stages of the cultivated mushroom Agaricus bisporus
  JOURNAL   Fungal Genet. Biol. 29 (2), 81-94 (2000)
  MEDLINE   20374017
   PUBMED   10919377
COMMENT     Contact: Manuel D. Ospina-Giraldo
            Mushroom Research Laboratory, Department of Plant Pathology
            The Pennsylvania State University
            305 Buckhout, University Park, PA 16802, USA
            Tel: 8148633073
            Fax: 8148637217
            Email: mxo11@psu.edu
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .56
                     /organism="Agaricus bisporus"
                     /mol_type="mRNA"
                     /strain="Sylvan-130"
                     /db_xref="taxon:5341"
                     /tissue_type="Basidiome"
                     /clone_lib="Basidiome cDNA library"
                     /note="Vector: pBluescript II SK (+); Site_1: SalI;
                     Site_2: NotI"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         12 CW 11


RESULT 83
AW444409
LOCUS       AW444409                  56 bp    mRNA    linear   EST 25-SEP-2000
DEFINITION  AB573 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA
            sequence.
ACCESSION   AW444409
VERSION     AW444409.1  GI:10282207
KEYWORDS    EST.
SOURCE      Agaricus bisporus
  ORGANISM  Agaricus bisporus
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
            Agaricales; Agaricaceae; Agaricus.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.
  TITLE     Classification of sequences expressed during the primordial and
            basidiome stages of the cultivated mushroom Agaricus bisporus
  JOURNAL   Fungal Genet. Biol. 29 (2), 81-94 (2000)
  MEDLINE   20374017
   PUBMED   10919377
COMMENT     Contact: Manuel D. Ospina-Giraldo
            Mushroom Research Laboratory, Department of Plant Pathology
            The Pennsylvania State University
            305 Buckhout, University Park, PA 16802, USA
            Tel: 8148633073
```

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            Fax: 8148637217
            Email: mxo11@psu.edu
            Seq primer: T7.
FEATURES                Location/Qualifiers
     source             1. .56
                        /organism="Agaricus bisporus"
                        /mol_type="mRNA"
                        /strain="Sylvan-130"
                        /db_xref="taxon:5341"
                        /tissue_type="Primordium"
                        /clone_lib="Primordium cDNA library"
                        /note="Vector: pBluescript II SK (+); Site_1: SalI;
                        Site_2: NotI"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         24 WG 25


RESULT 84
AW444409/c
LOCUS       AW444409                  56 bp    mRNA    linear   EST 25-SEP-2000
DEFINITION  AB573 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA
            sequence.
ACCESSION   AW444409
VERSION     AW444409.1  GI:10282207
KEYWORDS    EST.
SOURCE      Agaricus bisporus
  ORGANISM  Agaricus bisporus
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
            Agaricales; Agaricaceae; Agaricus.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Ospina-Giraldo,M.D., Collopy,P.D., Romaine,C.P. and Royse,D.J.
  TITLE     Classification of sequences expressed during the primordial and
            basidiome stages of the cultivated mushroom Agaricus bisporus
  JOURNAL   Fungal Genet. Biol. 29 (2), 81-94 (2000)
  MEDLINE   20374017
   PUBMED   10919377
COMMENT     Contact: Manuel D. Ospina-Giraldo
            Mushroom Research Laboratory, Department of Plant Pathology
            The Pennsylvania State University
            305 Buckhout, University Park, PA 16802, USA
            Tel: 8148633073
            Fax: 8148637217
            Email: mxo11@psu.edu
            Seq primer: T7.
FEATURES                Location/Qualifiers
     source             1. .56
                        /organism="Agaricus bisporus"
                        /mol_type="mRNA"
                        /strain="Sylvan-130"
                        /db_xref="taxon:5341"
                        /tissue_type="Primordium"
                        /clone_lib="Primordium cDNA library"
                        /note="Vector: pBluescript II SK (+); Site_1: SalI;
                        Site_2: NotI"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
              ||
Db         25 CW 24


RESULT 85
BG838323
LOCUS       BG838323                  56 bp    mRNA    linear   EST 25-MAY-2001
DEFINITION  Gc01_08e06_R Gc01_AAFC_ECORC_cold_stressed_Glycine_clandestina
            Glycine clandestina cDNA clone Gc01_08e06, mRNA sequence.
ACCESSION   BG838323
VERSION     BG838323.1  GI:14204645
KEYWORDS    EST.
SOURCE      Glycine clandestina
  ORGANISM  Glycine clandestina
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A.,
            Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and
            Tinker,N.A.
  TITLE     Expressed Sequence Tags from Cold-Stressed Glycine clandestina
            Seedlings
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@agr.gc.ca.
FEATURES                Location/Qualifiers
     source             1. .56
                        /organism="Glycine clandestina"
                        /mol_type="mRNA"
                        /cultivar="1035"
                        /db_xref="taxon:45687"
                        /clone="Gc01_08e06"
                        /tissue_type="Leaves, stem"
                        /clone_lib="Gc01_AAFC_ECORC_cold_stressed_Glycine_clandest
                        ina"
                        /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
                        Site_2: XhoI; Plants incubated at 2 degrees under 12 hours
                        of light/day.  Harvested  after only 2-3 days of cold
                        treatment. cDNA was prepared with the  Uni-Zap cDNA kit
                        from Stratagene.  Eco RI adapters were linked followed  by
                        digest with Xho I/Eco RI and ligated to pBluescript."
ORIGIN

  Query Match             20.0%;  Score 2;  DB 4;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         43 GY 44


RESULT 86
BG838323/c
LOCUS       BG838323                  56 bp    mRNA    linear   EST 25-MAY-2001
DEFINITION  Gc01_08e06_R Gc01_AAFC_ECORC_cold_stressed_Glycine_clandestina
            Glycine clandestina cDNA clone Gc01_08e06, mRNA sequence.
ACCESSION   BG838323
VERSION     BG838323.1  GI:14204645
KEYWORDS    EST.
SOURCE      Glycine clandestina
  ORGANISM  Glycine clandestina
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A.,
            Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and
            Tinker,N.A.
```

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  TITLE     Expressed Sequence Tags from Cold-Stressed Glycine clandestina
            Seedlings
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Singh,J.A.
            Eastern Cereal and Oilseed Research Centre
            Agriculture and Agri-food Canada
            KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
            0C6, Canada
            Tel: (613) 759-1662
            Fax: (613) 759-1701
            Email: singhja@agr.gc.ca.
FEATURES             Location/Qualifiers
     source          1. .56
                     /organism="Glycine clandestina"
                     /mol_type="mRNA"
                     /cultivar="1035"
                     /db_xref="taxon:45687"
                     /clone="Gc01_08e06"
                     /tissue_type="Leaves, stem"
                     /clone_lib="Gc01_AAFC_ECORC_cold_stressed_Glycine_clandest
                     ina"
                     /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
                     Site_2: XhoI; Plants incubated at 2 degrees under 12 hours
                     of light/day.  Harvested  after only 2-3 days of cold
                     treatment. cDNA was prepared with the  Uni-Zap cDNA kit
                     from Stratagene.  Eco RI adapters were linked followed  by
                     digest with Xho I/Eco RI and ligated to pBluescript."
ORIGIN

  Query Match             20.0%;  Score 2;  DB 4;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         44 RC 43


RESULT 87
CNS013GI
LOCUS       CNS013GI                  56 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN10D06 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL102828
VERSION     AL102828.1  GI:5614439
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .56
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN10D06"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         50 RC 51


RESULT 88
CNS013GI/c
LOCUS       CNS013GI                  56 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN10D06 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL102828
VERSION     AL102828.1  GI:5614439
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 56)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .56
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN10D06"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 56;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         51 GY 50


RESULT 89
CNS00BH8
LOCUS       CNS00BH8                  57 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR23G24 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL057073
VERSION     AL057073.1  GI:4937640
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 57)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
source 1. .57
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR23G24"
/clone_lib="RPCI-98"
/note="end : T7"
ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 57;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
||
Db 49 WG 50

RESULT 90
CNS00BH8/c
LOCUS CNS00BH8 57 bp DNA linear GSS 04-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC # BACR23G24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL057073
VERSION AL057073.1 GI:4937640
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 57)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
source 1. .57
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR23G24"
/clone_lib="RPCI-98"
/note="end : T7"
ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 57;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
||
Db 50 CW 49

RESULT 91
CNS0217V
LOCUS CNS0217V 57 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 224P22 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL176548
VERSION AL176548.1 GI:7814605
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 57)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES Location/Qualifiers
source 1. .57
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="224P22"
/clone_lib="G"

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                     /note="Genoscope sequence ID : C0AG224DH11LP1~end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         56 GY 57


RESULT 92
CNS0217V/c
LOCUS       CNS0217V                  57 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            224P22 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL176548
VERSION     AL176548.1  GI:7814605
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 57)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="224P22"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG224DH11LP1~end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         57 RC 56


RESULT 93
CNS02S8W
LOCUS       CNS02S8W                  57 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            161L21 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL211577
VERSION     AL211577.1  GI:7870396
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 57)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="161L21"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG161CF11LP1~end : T7"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
              ||
Db         48 RC 49


RESULT 94
CNS02S8W/c
LOCUS       CNS02S8W                  57 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            161L21 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL211577
VERSION     AL211577.1  GI:7870396
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
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  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 57)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .57
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
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                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG161CF11LP1~end : T7"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         49 GY 48


RESULT 95
CNS03R92
LOCUS       CNS03R92                   57 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            049I19 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL256943
VERSION     AL256943.1  GI:7977955
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 57)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="049I19"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG049AE10SP1~end :
                     PUC-Ori"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         51 WG 52


RESULT 96
CNS03R92/c
LOCUS       CNS03R92                   57 bp    DNA     linear   GSS 01-SEP-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            049I19 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL256943
VERSION     AL256943.1  GI:7977955
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetradontoidea; Tetraodontidae; Tetraodon.
REFERENCE   1
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
   PUBMED   10835645
REFERENCE   2
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
            Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
            Saurin,W., Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
```

```
  MEDLINE   20359837
   PUBMED   10899143
REFERENCE   3  (bases 1 to 57)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .57
                     /organism="Tetraodon nigroviridis"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:99883"
                     /clone="049I19"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG049AE10SP1~end :
                     PUC-Ori"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 57;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy          4 CW 5
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Db         52 CW 51


RESULT 97
AY439683
LOCUS       AY439683                  58 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Armigeres subalbatus ASAP ID: 39959 unknown mRNA sequence.
ACCESSION   AY439683
VERSION     AY439683.1  GI:42764713
KEYWORDS    HTC.
SOURCE      Armigeres subalbatus
  ORGANISM  Armigeres subalbatus
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Armigeres.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 58)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="Armigeres subalbatus"
                     /mol_type="mRNA"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:124917"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 39958"
     misc_feature    1. .58
                     /note="unknown; low quality sequence; ASAP-UW Feature ID:
                     39959"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 58;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
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Db         22 RC 23


RESULT 98
AY439683/c
LOCUS       AY439683                  58 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Armigeres subalbatus ASAP ID: 39959 unknown mRNA sequence.
ACCESSION   AY439683
VERSION     AY439683.1  GI:42764713
KEYWORDS    HTC.
SOURCE      Armigeres subalbatus
  ORGANISM  Armigeres subalbatus
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Armigeres.
REFERENCE   1  (bases 1 to 58)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 58)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .58
                     /organism="Armigeres subalbatus"
                     /mol_type="mRNA"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:124917"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
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     misc_feature    1. .58
                     /note="unknown; low quality sequence; ASAP-UW Feature ID:
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39959"
ORIGIN

Query Match 20.0%; Score 2; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4
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Db 46 RC 45

RESULT 99
AF211549
LOCUS AF211549 59 bp mRNA linear EST 31-DEC-2000
DEFINITION AF211549 34.1B Nicotiana tabacum cDNA clone fragment 9, mRNA sequence.
ACCESSION AF211549
VERSION AF211549.1 GI:11999941
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 59)
AUTHORS Durrant,W.E., Rowland,O., Piedras,P., Hammond-Kosack,K.E. and Jones,J.D.G.
TITLE cDNA expression profiling reveals rapid, resistance gene-dependent, active oxygen-independent, gene induction during the plant defence response
JOURNAL Unpublished (1999)
COMMENT Contact: Durrant WE
Sainsbury Laboratory
John Innes Centre
Colney Lane, Norwich, Norfolk NR4 7UH, UK
Email: wendy.durrant@bbsrc.ac.uk
rapidly induced, oxidative burst independent cDNA-AFLP fragment.
FEATURES Location/Qualifiers
source 1. .59
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/cultivar="Petite Havana"
/db_xref="taxon:4097"
/clone="fragment 9"
/clone_lib="34.1B"
/note="cell suspension cultures harvested 30 min after treatment with the Avr9 peptide from the fungus Cladosporium fulvum; 34.1B tobacco contains Cf-9 resistance gene"
ORIGIN

Query Match 20.0%; Score 2; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
||
Db 37 WG 38

RESULT 100
AF211549/c
LOCUS AF211549 59 bp mRNA linear EST 31-DEC-2000
DEFINITION AF211549 34.1B Nicotiana tabacum cDNA clone fragment 9, mRNA sequence.
ACCESSION AF211549
VERSION AF211549.1 GI:11999941
KEYWORDS EST.
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 59)
AUTHORS Durrant,W.E., Rowland,O., Piedras,P., Hammond-Kosack,K.E. and Jones,J.D.G.
TITLE cDNA expression profiling reveals rapid, resistance gene-dependent, active oxygen-independent, gene induction during the plant defence response
JOURNAL Unpublished (1999)
COMMENT Contact: Durrant WE
Sainsbury Laboratory
John Innes Centre
Colney Lane, Norwich, Norfolk NR4 7UH, UK
Email: wendy.durrant@bbsrc.ac.uk
rapidly induced, oxidative burst independent cDNA-AFLP fragment.
FEATURES Location/Qualifiers
source 1. .59
/organism="Nicotiana tabacum"
/mol_type="mRNA"
/cultivar="Petite Havana"
/db_xref="taxon:4097"
/clone="fragment 9"
/clone_lib="34.1B"
/note="cell suspension cultures harvested 30 min after treatment with the Avr9 peptide from the fungus Cladosporium fulvum; 34.1B tobacco contains Cf-9 resistance gene"
ORIGIN

Query Match 20.0%; Score 2; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
||
Db 38 CW 37

RESULT 101
AY439538
LOCUS AY439538 59 bp mRNA linear HTC 24-JUN-2004
DEFINITION Armigeres subalbatus ASAP ID: 42101 unknown mRNA sequence.
ACCESSION AY439538
VERSION AY439538.1 GI:42764563
KEYWORDS HTC.
SOURCE Armigeres subalbatus
ORGANISM Armigeres subalbatus
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Armigeres.
REFERENCE 1 (bases 1 to 59)
AUTHORS Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T., Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P., Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
TITLE Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres subalbatus
JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED 15213157
REFERENCE 2 (bases 1 to 59)
AUTHORS Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T., Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K., Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-2003) Animal Health and Biomedical Sciences, University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI 53706, USA
COMMENT More information about this sequence is available in ASAP (A Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at https://asap.ahabs.wisc.edu/annotation/php/logon.php.

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FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="Armigeres subalbatus"
                     /mol_type="mRNA"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:124917"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 42100"
     misc_feature    1. .59
                     /note="unknown; low quality sequence; ASAP-UW Feature ID:
                     42101"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
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Db         41 CW 42


RESULT 102
AY439538/c
LOCUS       AY439538                 59 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Armigeres subalbatus ASAP ID: 42101 unknown mRNA sequence.
ACCESSION   AY439538
VERSION     AY439538.1  GI:42764563
KEYWORDS    HTC.
SOURCE      Armigeres subalbatus
  ORGANISM  Armigeres subalbatus
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Armigeres.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 59)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="Armigeres subalbatus"
                     /mol_type="mRNA"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:124917"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 42100"
     misc_feature    1. .59
                     /note="unknown; low quality sequence; ASAP-UW Feature ID:
                     42101"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 WG 7
              ||
Db         42 WG 41


RESULT 103
CNS0111A
LOCUS       CNS0111A                 59 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN05J19 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL099688
VERSION     AL099688.1  GI:5611299
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN05J19"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : SP6"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RR 2
              ||
Db         43 RR 44


RESULT 104
CNS0111A/c
LOCUS       CNS0111A                 59 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN05J19 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL099688
VERSION     AL099688.1  GI:5611299
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KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
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                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN05J19"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : SP6"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YY 9
              ||
Db         44 YY 43


RESULT 105
CNS014IM
LOCUS       CNS014IM                  59 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN11G20 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL104200
VERSION     AL104200.1  GI:5615811
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN11G20"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : SP6"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WW 6
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Db         56 WW 57


RESULT 106
CNS014IM/c
LOCUS       CNS014IM                  59 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN11G20 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL104200
VERSION     AL104200.1  GI:5615811
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 59)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .59
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:7227"
                     /clone="BACN11G20"
                     /clone_lib="DrosBAC"
                     /plasmid="pBeloBAC11"
                     /note="end : SP6"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 9;  Length 59;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 WW 6
              ||
Db         57 WW 56


RESULT 107
AW059629
LOCUS       AW059629                  60 bp    mRNA    linear   EST 23-AUG-2000
DEFINITION  HuTH.bsst.dnc15.final.cluster_119_(2) DNC15 Homo sapiens cDNA
            similar to KIAA0741, mRNA sequence.
ACCESSION   AW059629
VERSION     AW059629.1  GI:6651951
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
            McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
            Burcham,T. and Albrecht,G.
  TITLE     In vitro cloning of complex mixtures of DNA on microbeads: Physical
            separation of differentially expressed cDNAs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
  MEDLINE   20144098
   PUBMED   10677516
COMMENT     Contact: Burcham TS
            LYNX Therapeutics, Inc.
            25861 Industrial Blvd., Hayward, CA 94545, USA
            Tel: 510 670 9338
            Fax: 510 670 9302
            Email: timb@lynxgen.com
            Sequence obtained from LYNX Therapeutics Megasort technology.
            Collected from the down-regulated gate. Consensus sequence of 2
            sequences in cluster.
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocyctic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="DNC15"
                     /note="Vector: pCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of down-regulated cDNA. THP-1
                     cells non-induced (treated with DMSO only). "
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
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Db         17 RC 18


RESULT 108
AW059629/c
LOCUS       AW059629                  60 bp    mRNA    linear   EST 23-AUG-2000
DEFINITION  HuTH.bsst.dnc15.final.cluster_119_(2) DNC15 Homo sapiens cDNA
            similar to KIAA0741, mRNA sequence.
ACCESSION   AW059629
VERSION     AW059629.1  GI:6651951
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Brenner,S., Williams,S.R., Vermass,E.H., Storck,T., Moon,K.,
            McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
            Burcham,T. and Albrecht,G.
  TITLE     In vitro cloning of complex mixtures of DNA on microbeads: Physical
            separation of differentially expressed cDNAs
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
  MEDLINE   20144098
   PUBMED   10677516
COMMENT     Contact: Burcham TS
            LYNX Therapeutics, Inc.
            25861 Industrial Blvd., Hayward, CA 94545, USA
            Tel: 510 670 9338
            Fax: 510 670 9302
            Email: timb@lynxgen.com
            Sequence obtained from LYNX Therapeutics Megasort technology.
            Collected from the down-regulated gate. Consensus sequence of 2
            sequences in cluster.
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_type="monocyctic leukemia"
                     /cell_line="THP-1 (TIB-202)"
                     /clone_lib="DNC15"
                     /note="Vector: pCR2.1; Cloning of PCR products from
                     micro-beads carrying 3' end of down-regulated cDNA. THP-1
                     cells non-induced (treated with DMSO only). "
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
              ||
Db         18 GY 17


RESULT 109
AW582843
LOCUS       AW582843                  60 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  top3g66 Neuronal Differentiation of the NT2/D1 cell line. Homo
            sapiens cDNA 3' similar to EST, mRNA sequence.
ACCESSION   AW582843
VERSION     AW582843.1  GI:7382089
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Bevort,M.
  TITLE     Analysis of gene expression during neuronal differentiation of
            NT2/D1 cells
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Bevort M
            Department of Growth and Reproduction GR-5064
            Copenhagen University Hospital
            Blegdamsvej 9, 2100 Copenhagen, Denmark
            Tel: +45 35455081
            Fax: +45 35456054
            Email: maja@biobase.dk
            The EST's expression level is constant, during neuronal
            differentiation of the NT2/D1 cell line (replated fully
            differentiated neurones not analysed).
            PCR PRimers
            FORWARD: GGCCTTCTTGTGT
            BACKWARD: AAGCTTTTTTTTTTG
            Seq primer: T7, CY5-TAATACGACTCACTATAGGGCC
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="NT2/D1"
                     /clone_lib="Neuronal Differentiation of the NT2/D1 cell
                     line."
                     /note="The EST is derived from direct sequencing of a
                     Differential  Display fragment. Laboratory manuals are
                     available from  http//www.biobase.dk/~ddbase"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RR 2
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Db         40 RR 41


RESULT 110
AW582843/c
LOCUS       AW582843                 60 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  top3g66 Neuronal Differentiation of the NT2/D1 cell line. Homo
            sapiens cDNA 3' similar to EST, mRNA sequence.
ACCESSION   AW582843
VERSION     AW582843.1  GI:7382089
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Bevort,M.
  TITLE     Analysis of gene expression during neuronal differentiation of
            NT2/D1 cells
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Bevort M
            Department of Growth and Reproduction GR-5064
            Copenhagen University Hospital
            Blegdamsvej 9, 2100 Copenhagen, Denmark
            Tel: +45 35455081
            Fax: +45 35456054
            Email: maja@biobase.dk
            The EST's expression level is constant, during neuronal
            differentiation of the NT2/D1 cell line (replated fully
            differentiated neurones not analysed).
            PCR PRimers
            FORWARD: GGCCTTCTTGTGT
            BACKWARD: AAGCTTTTTTTTTTTG
            Seq primer: T7, CY5-TAATACGACTCACTATAGGGCC
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="NT2/D1"
                     /clone_lib="Neuronal Differentiation of the NT2/D1 cell
                     line."
                     /note="The EST is derived from direct sequencing of a
                     Differential  Display fragment. Laboratory manuals are
                     available from  http//www.biobase.dk/~ddbase"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 2;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 YY 9
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Db         41 YY 40


RESULT 111
AY432469
LOCUS       AY432469                 60 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 36119 unknown mRNA sequence.
ACCESSION   AY432469
VERSION     AY432469.1  GI:42762639
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 60)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 36118"
     misc_feature    1. .60
                     /note="unknown; ASAP-UW Feature ID: 36119"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 RC 4
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Db         50 RC 51


RESULT 112
AY432469/c
LOCUS       AY432469                 60 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 36119 unknown mRNA sequence.
ACCESSION   AY432469
VERSION     AY432469.1  GI:42762639
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 60)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
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            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 36118"
     misc_feature    1. .60
                     /note="unknown; ASAP-UW Feature ID: 36119"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 GY 8
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Db         51 GY 50


RESULT 113
AY432601
LOCUS       AY432601                  60 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 37053 unknown mRNA sequence.
ACCESSION   AY432601
VERSION     AY432601.1  GI:42763838
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 60)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
                     /sex="female"
                     /cell_type="hemocyte"
                     /tissue_type="hemolymph"
                     /dev_stage="adult"
                     /note="ASAP-UW Feature ID: 37052"
     misc_feature    1. .60
                     /note="unknown; ASAP-UW Feature ID: 37053"
ORIGIN

  Query Match             20.0%;  Score 2;  DB 3;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 CW 5
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Db         27 CW 28


RESULT 114
AY432601/c
LOCUS       AY432601                  60 bp    mRNA    linear   HTC 24-JUN-2004
DEFINITION  Aedes aegypti ASAP ID: 37053 unknown mRNA sequence.
ACCESSION   AY432601
VERSION     AY432601.1  GI:42763838
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
  ORGANISM  Aedes aegypti
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1  (bases 1 to 60)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
  TITLE     Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
  JOURNAL   Infect. Immun. 72 (7), 4114-4126 (2004)
   PUBMED   15213157
REFERENCE   2  (bases 1 to 60)
  AUTHORS   Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="Aedes aegypti"
                     /mol_type="mRNA"
                     /strain="liverpool"
                     /isolation_source="perfused hemolymph of
                     bacteria-innoculated organisms at 1, 3, 6, 12, and 24
                     hours post-innoculation"
                     /db_xref="taxon:7159"
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